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OM nucleic - nucleic search, using sw model

Run on: December 29, 2004, 13:38:09 ; Search time 2260 Seconds  
(without alignments)  
9353.317 Million cell updates/sec

Title: US-09-851-138C-51

Perfect score: 447  
Sequence: 1 gacggaatttcgaatttcgaac.....aggactgcacgttcacac 447

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

GenBank: 1: gb\_ba: 2: gb\_hg: 3: gb\_in: 4: gb\_cm: 5: gb\_ov: 6: gb\_pat: 7: gb\_ph: 8: gb\_pl: 9: gb\_pr: 10: gb\_ro: 11: gb\_sb: 12: gb\_sy: 13: gb\_un: 14: gb\_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	445.8	99.7	447	6 A50396	A50396 Sequence 51
2	445.8	99.7	447	6 AR127536	AR127536 Sequence
3	445.8	99.7	447	14 HPCORREB	L39317 Hepatitis C
4	393	87.9	1584	14 HPCURK049A5	D49749 Hepatitis C
5	393	87.9	1584	14 HPCURK055A6	D49750 Hepatitis C
6	393	87.9	1584	14 HPCURK070A8	D49752 Hepatitis C
7	393	87.9	1584	14 HPCURK049R1	D49747 Hepatitis C
8	389.8	87.2	1584	14 HPCURK030A3	D49745 Hepatitis C
9	388.2	86.8	1584	14 HPCURK072A9	D49753 Hepatitis C
10	322.8	72.2	411	14 HPCCP3	D30046 Hepatitis C
11	255.8	57.2	1505	14 HPCNBE125C	D16614 Hepatitis C
12	252.2	56.4	1505	14 HPCNBE274I	D16620 Hepatitis C
13	244.4	54.7	1504	14 HPCNBE048A	D16618 Hepatitis C
14	241.2	54.0	1504	14 HPCNBE137E	D16616 Hepatitis C
15	239.4	53.6	1504	14 HPCNBE137E	D16616 Hepatitis C
16	238.2	53.3	1504	14 HPCNBE145G	D16618 Hepatitis C
17	236.6	52.9	1504	14 HPCNBE048A	D16618 Hepatitis C
18	236.4	52.9	867	14 HPCNBE048A	D16618 Hepatitis C
19	236.2	52.8	541	6 A40613	A40613 Sequence 13

20	236.2	52.8	541	6 A40617	A40617 Sequence 17
21	236.2	52.8	541	6 AX031591	AX031591 Sequence
22	236.2	52.8	541	6 AX031595	AX031595 Sequence
23	236.2	52.8	541	6 AX031861	AX031861 Sequence
24	236.2	52.8	541	6 AX031865	AX031865 Sequence
25	236.2	52.8	541	6 AX032131	AX032131 Sequence
26	236.2	52.8	541	6 AX032135	AX032135 Sequence
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34	234.6	52.5	541	6 AX032137	AX032137 Sequence
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38	233	52.1	541	6 A40615	A40615 Sequence 15
39	233	52.1	541	6 A40621	A40621 Sequence 21
40	233	52.1	541	6 A40625	A40625 Sequence 25
41	233	52.1	541	6 A40627	A40627 Sequence 27
42	233	52.1	541	6 AX031593	AX031593 Sequence
43	233	52.1	541	6 AX031599	AX031599 Sequence
44	233	52.1	541	6 AX031603	AX031603 Sequence
45	233	52.1	541	6 AX031605	AX031605 Sequence

#### ALIGNMENTS

RESULT 1	A50396	447 bp	DNA	linear	PAT 07-MAR-1997
LOCUS	A50396	Sequence 51 from Patent WO9613590.			
DEFINITION	A50396				
ACCESSION	A50396				
VERSION	A50396.1	GI:2303407			
KEYWORDS	unclassified				
SOURCE	unclassified				
ORGANISM	unclassified				
REFERENCE	1 (bases 1 to 447)				
AUTHORS	Maertens G. and Stuyver L.				
TITLE	NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC AGENTS				
JOURNAL	Patent: WO 9613590-A 51 09-MAY-1996;				
COMMENT	INNOVEMETICS NV. (BE)				
FEATURES	Other publication AU 3844095 960523.				
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Best Local Similarity	100.0%; Pred. No. 9.5e-109; Indels 0; Gaps 0;				
Matches 447; Conservative 0; Mismatches 0;					
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DB	1 GACGGATTAATTGCGACAGGGAATTACCGTGGCTCTTCTCTATCTCTCTG 60				
QY	61 GCTTGTCTCAAGCTGCTTACACCCAGCGGCTGAGTACCGTATGCTTCGGA 120				
DB	61 GCTTGTCTCAAGCTGCTTACACCCAGCGGCTGAGTACCGTATGCTTCGGA 120				
QY	121 CTCCTACATGTAACGTAACGTAACGTAACGTAACGTAACGTAACGTAACGTA 180				
DB	121 CTCCTACATGTAACGTAACGTAACGTAACGTAACGTAACGTAACGTAACGTA 180				
QY	181 ATCCCTCACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240				
DB	181 ATCCCTCACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240				

Db	181	ATCCTCCACCTTAACCTGGCGCTGATGCCCTTCGCGTAAGCCTCTGGCAATATACATGAAGATGCTGG	240
Qy	241	ATCCCTGTGAGGCCCTCYAACCGCTGCGCGGTGAAGTGCCCTGCGCGCCAGCCGCTCTCTCCGC	300
Db	241	ATCCCTGTGAGGCCCTCYAACCGCTGCGCGGTGAAGTGCCCTGCGCGCCAGCCGCTCTCTCCGC	300
Qy	301	ACGCACCTGTGAAATATATGTGTGGGRRCCGCGCACCCCTATATGTCTCAGCTCTCTTAGATAGAAAC	360
Db	301	ACGCACCTGTGAAATATATGTGTGGGRRCCGCGCACCCCTATATGTCTCTACGTCTTAGAGAAAC	360
Qy	361	CTTTGTGAGAGCGCTATTTCTTGTGTGGGAGGGGTTCTGATGAGACATCGCAGCATTTGG	420
Db	361	CTTTGTGAGAGCGCTATTTCTTGTGTGGGAGGGGTTCTGATGAGACATCGCAGCATTTGG	420
Qy	421	ACTGTCCAGGACTGCACACTGTTCCATC	447
Db	421	ACTGTCCAGGACTGCACACTGTTCCATC	447
RESULT 2			
LOCUS	AR127536	447 bp	DNA
DEFINITION	Sequence 51 from patent US 6180768.	linear	PAT 16-MAY-2001
ACCESSION	AR127536		
VERSION	AR127536.1	GI:14114131	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 447)		
TITLE	Maertens,G. and Stuyver,L.		
JOURNAL	Sequences of hepatitis C virus genotypes and their use as		
FEATURES	prophylactic, therapeutic and diagnostic agents		
source	Patent: US 6180768-A 51 30 -JAN-2001;		
	Location/Qualifiers		
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ORIGIN	/mol_type="unassigned DNA"		
Query Match	99.7%; Score 445.8; DB 6; Length 447;		
Best Local Similarity	100.0%; Pred. No. 9.5e-109;		
Matches	447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	GACGGAAATTAATTTGCAACAGGGAATTTACCTGGTGTGCTCTTCTCTATCTTCTCTCG	60
Db	1	GACGGAAATTAATTTGCAACAGGGAATTTACCTGGTGTGCTCTTCTCTATCTTCTCTCG	60
Qy	61	GCTTGTGTTCTCATGCTTGCTTACACCCACAGCGGGCTGAGATACCGTAATGCTCCGGA	120
Db	61	GCTTGTGTTCTCATGCTTGCTTACACCCACAGCGGGCTGAGATACCGTAATGCTCCGGA	120
Qy	121	CTTACATGATGTAACTAAGACGTGACGTAAACGCTATATCGTATGAGAGCCGGGATATT	180
Db	121	CTTACATGATGTAACTAAGACGTGACGTAAACGCTATATCGTATGAGAGCCGGGATATT	180
Qy	181	ATCCTCCACTTAACCTGCTGTGTCCCTGCGTACGCTCTGCAATATATCAAGATGCTGG	240
Db	181	ATCCTCCACTTAACCTGCTGTGTCCCTGCGTACGCTCTGCAATATATCAAGATGCTGG	240
Qy	241	ATCCCTGAGAGCCCTAACCGTGGCGGTGAAGTGGCCCTGCGCCGACCGCTCTTCTCCGC	300
Db	241	ATCCCTGAGAGCCCTAACCGTGGCGGTGAAGTGGCCCTGCGCCGACCGCTCTTCTCCGC	300
Qy	301	ACGACCTGTGAAATATATGTGTGGGRRCCGCGCACCCCTATCTCTTACGTAGAGAAC	360
Db	301	ACGACCTGTGAAATATATGTGTGGGRRCCGCGCACCCCTATCTCTTACGTAGAGAAC	360
Qy	361	CTTTGTGAGAGCGCTATTTCTTGTGTGGGAGGGGTTCTGATGAGACATCGCAGCATTTGG	420
Db	361	CTTTGTGAGAGCGCTATTTCTTGTGTGGGAGGGGTTCTGATGAGACATCGCAGCATTTGG	420
Qy	421	ACTGTCCAGGACTGCACACTGTTCCATC	447

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Db      181 ATCCCTCACTTACCTGGCTGTGTCCCTGCGTACGCTCTGGCAATACATCAAGATGTGG 240
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Db      241 ATCCCTGTGTAGCCCTTACCGTGCCTGGAAGTGCCTTGCCTGCGCCACCGCTTCTTCCG 300
Qy      301 AGCAGCTGTGATATGATGTGGAGGCGGCCACCTATGCTCACTCTCTAAGTAGAGAC 360
Db      301 AGCAGCTGTGATATGATGTGGAGGCGGCCACCTATGCTCACTCTCTAAGTAGAGAC 360
Qy      361 CTTTGTGAGCGCTATTTCTTGTGGGACAGGGGTTCTCATGAGACATCGCCAGCATTTG 420
Db      361 CTTTGTGAGCGCTATTTCTTGTGGGAGGGGTTCTCATGAGACATCGCCAGCATTTG 420
Qy      421 ACTGTCCAGAGCTGCAACTGTTCCATC 447
Db      421 ACTGTCCAGAGCTGCAACTGTTCCATC 447

RESULT 4
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LOCUS           Hepatitis C virus isolate JK049 gene for core, env, and part of
DEFINITION      E2/NS1, partial cds.
ACCESSION       D49749.1 GI:1197110
VERSION         D49749
KEYWORDS        core, env, and part of E2/NS1.
SOURCE          Hepatitis C virus
ORGANISM        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                Hepacivirus.
REFERENCE       1 (sites)
AUTHORS         Tokita,H., Okamoto,H., Iizuka,H., Kishimoto,J., Tsuda,F.,
                Lesmana,L.A., Miyakawa,Y. and Mayumi,M.
TITLE           Hepatitis C virus variants from Jakarta, Indonesia classifiable
                into novel genotypes in the second (2e and 2f), tenth (10a) and
                eleventh (11a) genetic groups
JOURNAL         J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
MEDLINE         96226020
PUBMED          8627233
REFERENCE       2 (bases 1 to 1584)
AUTHORS         Okamoto,H.
JOURNAL         Unpublished
REFERENCE       3 (bases 1 to 1584)
AUTHORS         Okamoto,H.
TITLE           Direct Submision
JOURNAL         Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
                Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
                329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
                Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
FEATURES        Location/Qualifiers
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ORIGIN          ASGAFITSLFSTGAQPLHLVN"
Query Match     87.9%; Score 393; DB 14; Length 1584;
Best Local Similarity 91.9%; Pred. No.1.5e-94;
Matches 411; Conservative 3; Mismatches 33; Indels 0; Gaps 0;

Qy      1 GACGGAATTAATTTGGCAACAGGAATTACTGATGCTCTTCTCTATCTTCTTCG 60
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Qy      61 GCTTGTCTCATGTCTTGTCTTACACCAAGCGGAGTGAAGTACGTAATCCTCCGA 120
Db      877 GCTTGTCTCATGTCTTGTCTTACACCAAGCGGAGTGAAGTATGTAATCCTCCGA 936
Qy      121 CTCTACATGTATACACACGACGTAACGGTAGATGCTGTATGAGCGCGGATATT 180
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Qy      421 ACTGTCCAGAGCTGCAACTGTTCCATC 447
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RESULT 5
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LOCUS           Hepatitis C virus isolate JK055 gene for core, env, and part of
DEFINITION      E2/NS1, partial cds.
ACCESSION       D49750.1 GI:1197114
VERSION         D49750
KEYWORDS        core, env, and part of E2/NS1.
SOURCE          Hepatitis C virus
ORGANISM        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                Hepacivirus.
REFERENCE       1 (sites)
AUTHORS         Tokita,H., Okamoto,H., Iizuka,H., Kishimoto,J., Tsuda,F.,
                Lesmana,L.A., Miyakawa,Y. and Mayumi,M.
TITLE           Hepatitis C virus variants from Jakarta, Indonesia classifiable
                into novel genotypes in the second (2e and 2f), tenth (10a) and
                eleventh (11a) genetic groups
JOURNAL         J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
MEDLINE         96226020
PUBMED          8627233
REFERENCE       2 (bases 1 to 1584)
AUTHORS         Okamoto,H.
JOURNAL         Unpublished
REFERENCE       3 (bases 1 to 1584)
AUTHORS         Okamoto,H.
TITLE           Direct Submision
JOURNAL         Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School,
                Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi
                329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
                Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
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Query Match	87.9%;	Score 393;	DB 14;	Length 1584;
Best Local Similarity	91.9%;	Pred. No. 1.5e-94;		
Matches 411;	Conservative 3;	Mismatches 33;	Indels 0;	Gaps 0;

OY	1	GACGGAAATTAAATTTCGAAACAGGGAAATTACTGCTGGTCTCTTTCTCTAATTCTCCTTCG	60
Db	817	GACGGAAATCAATTTCGACACAGGGAATTACTGGTGTCTCTTTCTCTAATTCTTCTCTTG	876
OY	61	GCTTGTGTTCTCATGCTTGCTCTTACAACCCACAGCCGGGCTGAGTACCGTAAATGCCCTCGGA	120
Db	877	GCTTGTGTTCTCATGCTTGCTCTTACAACCCACAGCCGGGCTGAGTACCGTAAATGCCCTCGGA	936
OY	121	CTTTCATATGTGTAATCTAACGACTGCAAGTAAACGGTAACTATCGTGTATGAGGCGGGGAAATTT	180
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Db	1177	CTTTGTGGAGCGCTGTCTTTCTTTGTGTGGGAGAGGGTTCTCATGAGAACATTCGCACATTTGG	1236
OY	421	ACTGTCCAGACTGCAACTGTTCCATC	447
Db	1237	ACTGTCCAGACTGCAACTGTTCCATC	1263

RESULT 6	
HPVJK070A8	
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DEFINITION	Hepatitis C virus isolate JK070 gene for core, env, and part of E2/NS1, partial cds.
ACCESSION	D49752
VERSION	D49752.1 GI:1197162
KEYWORDS	core, env, and part of E2/NS1.
SOURCE	Hepatitis C virus
ORGANISM	Hepatitis C virus
	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirinae.

REFERENCE	1 (sites)
AUTHORS	Tohtite, H., Okamoto, H., Iizuka, H., Kishimoto, J., Tsuda, F., Lemana, U.A., Miyakawa, Y. and Megumi, M.
TITLE	Hepatitis C virus variante from Jakarta, Indonesia classified into novel genotypes in the second (2e and 2f), tenth (10a) and eleventh (11a) genetic groups
JOURNAL	J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
MEDLINE	96226020
PMID	8627233
REFERENCE	2 (bases 1 to 1584)
AUTHORS	Okamoto, H.
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 1584)
AUTHORS	Okamoto, H.
TITLE	Direct Submission
JOURNAL	Submitted (17-MAR-1995) Hiroaki Okamoto, Jichi Medical School, Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi 329-04, Japan (E-mail: hokamoto@jichi.ac.jp) Tel: 0285-44-2111 (ex.3334), Fax: 0285-44-1557)
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Query Match	87.9%;	Score 393;	DB 14;	Length 1584;
Best Local Similarity	91.9%;	Pred. No. 1.5e-94;		
Matches 411; Conservative	3;	Mismatches 33;	Indels 0;	Gaps 0;

Qy	1	GACGAAATTAATTTGGACAAGGGAAATTTACGTGTGCTCTTCTCTATCTTCCCTCTG	60
Db	817	GACGAAATCAATTTTGGACAAAGGGAATTTACCTGGTTGCTCTTCTCTATCTTCTCTG	876
Qy	61	GCTTGTATCATGCTGTGCTTACACCCAGCCGGGCTGGAGTACCGTAAAGCTCCGGA	120
Db	877	GCTTGTCTCTCAATGCTTGTCTTACACCCAGCCGGGCTGGAGTACCGTAAATGTCCTCGGA	936
Qy	121	CTTACATGAGTAACTAACGACTGAGTAAAGGTAATCTGTATATAGAGCCGGGGATATT	180
Db	937	CTTACATAGTAAACAAACGACTGAGTAAAGCAGTATTTGTATATAGAGCCGGGGATATT	996
Qy	181	ATCTCCACTTAACCTGGCTGTGTCCCTCGGTAACGCTTGAGCAATATCAATGAATGCTGG	240
Db	997	ATCTCCACTTGCCTGGCTGTGTCCCTCGGTAACGCTTGAGCAATATCAATGAATGTTGG	1056
Qy	241	ATCCCTGTGAGCCCTAACCGTCCGCGTGAATGCGCCTTGCGCCGACCGCCTCTCTCCG	300
Db	1057	ACCCTCTTAAGCCCTAACCGTCCGCGTGAATGCGCCTTGCGCCGCTCTCTCTCCG	1116
Qy	301	ACGCACTGATATATGATGTGGAGGAGCGGCAACCTTAATGCTCAACTCTCTAAGTAGAGAC	360
Db	1117	ACGCAATGATATATGATGTGGAGGAGCGGCAACCTTAATGCTCAACTCTCTAATGTAAGGAT	1176

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QY 361 CTTGTGGAGCGCTATTCTTGTGGGCGAGGGTTCATGAGACATGCGCAGCATTTGG 420
Db 1177 CTTGTGGAGCGCTATTCTTGTGGGCGAGGGTTCATGAGACATGCGCAGCATTTGG 1236
QY 421 ACTGTCAGAGCTCAACTGTTTCATC 447
Db 1237 ACTGTCAGAGCTCAACTGTTTCATC 1263

RESULT 7
HPCJK049E1 9450 bp RNA linear VRL 13-FEB-1999
LOCUS Hepatitis C virus isolate JKO49 genomic RNA for polyprotein,
DEFINITION complete genome.
ACCESSION D63821.1 GI:1183032
VERSION D63821.1
KEYWORDS polyprotein.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
vireuses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases)
AUTHORS Tokita,H., Okamoto,H., Itzuka,H., Kishimoto,J., Tenda,F.,
Lesmana,L.A., Miyakawa,Y. and Mayumi,M.
Hepatitis C virus variants from Jakarta, Indonesia classifiable
into novel genotypes in the second (2e and 2f), tenth (10a) and
eleventh (11a) genetic groups
J. Gen. Virol. 77 (Pt 2), 293-301 (1996)
JOURNAL 96226020
MEDLINE 8627233
PUBMED
REFERENCE 2 (bases 1 to 9450)
AUTHORS Okamoto,H.
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 9450)
AUTHORS Okamoto,H.
JOURNAL Direct Submission
Submitted (10-AUG-1995) Hiroaki Okamoto, Jichi Medical School,
Immunology Division, Minamikawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail:hokamoc@jichi.ac.jp),
Tel.:0285-44-2111 (ex.3334), Fax:0285-44-1557)
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Db	1177	CTTTGTGGAGCGCTATTTCTTGTGTGGCGAGGCGTTCTCATGAGACATCGCCACGATTGG		12368
Qy	421	ACTGTCCAGGAGCTGCACCTGTTCCATC	447	
Db	1237	ACTGTCCAGGAGTGCACCTGTTGCATC	1263	
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LOCUS		1584 bp	RNA	linear
DEFINITION		Hepatitis C virus isolate UK030 gene for core, env, and part of		
ACCESSION		E2/NS1, partial cds.		
VERSION		D49747		
KEYWORDS		core, env, and part of E2/NS1.		
SOURCE		Hepatitis C virus		
ORGANISM		Hepatitis C virus		
REFERENCE		Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.		
AUTHORS		1 (sites)		
TITLE		Tokita,H., Okamoto,H., Iizuka,H., Kishimoto,J., Tsuda,F.,		
JOURNAL		Lesmana,L.A., Miyakawa,Y. and Mayumi,M.		
REFERENCE		Hepatitis C virus variants from Jakarta, Indonesia classifiable		
AUTHORS		into novel genotypes in the second (2e and 2f), tenth (10a) and		
REFERENCE		eleventh (11a) genetic groups		
TITLE		J. Gen. Virol. 77 (Pt 2), 293-301 (1996)		
JOURNAL		96226020		
MEDLINE		8627233		
PUBMED		2 (bases 1 to 1584)		
REFERENCE		Okamoto,H.		
AUTHORS		Unpublished		
JOURNAL		3 (bases 1 to 1584)		
REFERENCE		Okamoto,H.		
TITLE		Direct Submission		
JOURNAL		Submitted (17-MAR-1995) Hiroaki Okamoto, Yichi Medical School,		
REFERENCE		Immunology Division, Minamikawachi-machi, Kawachi-gun, Tochigi		
AUTHORS		329-04, Japan (E-mail: hokamoto@jiichi.ac.jp.		
JOURNAL		Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)		
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			Gaps	0;
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Db	877	GCTTTGCTCTCATCTGCTTACACCCGACCGGGTTGAGTACCGTATGCTCCGGA	936			
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Db	937	CTTCAACATGTTACCTAACACTGACATGATCGGTATCGTATGAGGGCCGGGATATT	996			
QY	181	ATTCCTCCACTTACCGGAGTGTGTCCCTCGGCTGACGCTCTGACAAATCAAGATGCTGG	240			
Db	997	ATTCCTCCACTTACCGGAGTGTGTCCCTCGGCTGACGCTCTGACAAATCAAGATGCTGG	1056			
QY	241	ATTCCTGAGACCCCTGACCGCTGACCGCTGACCGCTGACCGCTGACCGCTGACCGC	300			
Db	1057	ATTCCTGAGACCCCTGACCGCTGACCGCTGACCGCTGACCGCTGACCGCTGACCGC	1116			
QY	301	ACGACATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	360			
Db	1117	ACGACATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1176			
QY	361	CTTGTGAGAGCGATTTCTTGTGAGGACGAGGCTTCATGAGACATTCGACGATTTGG	420			
Db	1177	CTTGTGAGAGCGATTTCTTGTGAGGACGAGGCTTCATGAGACATTCGACGATTTGG	1236			
QY	421	ACTGTCCAGACTCAACTGTTCATC	447			
Db	1237	ACTGTCCAGACTCAACTGTTCATC	1263			
RESULT 9	HEPCJK072A9	1584 bp RNA linear VRL 10-FEB-1999				
LOCUS	HEPCJK072A9	1584 bp RNA linear VRL 10-FEB-1999				
DEFINITION	Hepatitis C virus isolate JX072 gene for core, env, and part of E2/NS1, partial cde.					
VERSION	D49753.1	GI:1197124				
KEYWORDS	core, env, and part of E2/NS1.					
SOURCE	Hepatitis C virus					
ORGANISM	Hepatitis C virus					
REFERENCE	Vinuesa; ssRNA positive-strand viruses, no DNA stage; Flaviviridae, Hepacivirus.					
AUTHORS	1 (sites)					
TITLE	Tokita, H., Okamoto, H., Iizuka, H., Kishimoto, J., Tsuda, F., Iemama, L.A., Miyakawa, Y., and Mayumi, M.					
JOURNAL	Hepatitis C virus variants from Jakarta, Indonesia classifiable into novel genotypes in the second (2e and 2f), tenth (10a) and eleventh (11a) genetic groups					
MEDLINE	J. Gen. Virol. 77 (Pt 2), 293-301 (1996)					
PUBMED	96226020					
REFERENCE	8627233					
AUTHORS	2 (bases 1 to 1584)					
JOURNAL	Okamoto, H.					
REFERENCE	Unpublished					
AUTHORS	3 (bases 1 to 1584)					
TITLE	Okamoto, H.					
JOURNAL	Direct Submission					
FEATURES	Submitted (17-MAR-1995) Hiroaki Okamoto, Tichi Medical School, Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochigi 329-04, Japan [E-mail: hokamoto@ichi.ac.jp, Tel: 0285-44-2111 (ex.3334), Fax: 0285-44-1557]					
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VERSION D16614.1 GI:475866  
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ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
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REFERENCE  
AUTHORS 1 (sites)  
TITLE Tanaka, S.M., Tsuda, F., Okamoto, H., Tokita, H., Horikita, M.,  
Iizuka, H., Shrestha, S., Miyakawa, Y., and Mayumi, M.  
Hepatitis B virus subtypes and hepatitis C virus genotypes in  
patients with chronic liver disease in Nepal  
J. Gen. Virol. 75 (Pt 4), 931-936 (1994)  
JOURNAL Hepatology 19 (4), 805-809 (1994)  
MEDLINE 9418615  
PUBMED 8138250  
REFERENCE  
AUTHORS 2 (sites)  
TITLE Tokita, H., Shrestha, S.M., Okamoto, H., Sakamoto, M., Horikita, M.,  
Iizuka, H., Shrestha, S., Miyakawa, Y., and Mayumi, M.  
Hepatitis C virus variants from Nepal with novel genotypes and  
their classification into the third major group  
J. Gen. Virol. 75 (Pt 4), 931-936 (1994)  
JOURNAL 94201770  
MEDLINE 8151307  
PUBMED  
COMMENT Submitted (06-JUN-1993) to DDBJ by:  
Hiroaki Okamoto  
Immunology Division  
Jichi Medical School  
Kawachi-gun  
Tochigi-ken 329-04  
Japan  
Phone: 0285-44-2111 x3334  
Fax: 0285-44-1557.  
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ORIGIN  
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Best Local Similarity 73.6%; Pred. No. 1e-57;  
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QY 361 CTTGTGAGAGGCTATTTCTGTGTGGGAGGCTTCTATGAGATCGCAGCATTTGG 420  
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QY 421 ACTGTCCAGACTGCACTGTTC 443  
DB 1158 ACCGTCCAGTGTGCAATTTGCTC 1180  
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DEFINITION Hepatitis C virus RNA for core, env, and part of E2/NS1 polypeptide.  
ACCESSION D16620  
VERSION D16620.1 GI:475878  
KEYWORDS E2/NS1; core protein; envelope protein.  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepcivirinae.  
REFERENCE  
AUTHORS 1 (sites)  
TITLE Tanaka, S.M., Tsuda, F., Okamoto, H., Tokita, H., Horikita, M.,  
Tanaka, T., Miyakawa, Y., and Mayumi, M.  
Hepatitis B virus subtypes and hepatitis C virus genotypes in  
patients with chronic liver disease in Nepal  
Hepatology 19 (4), 805-809 (1994)  
JOURNAL 9418615  
MEDLINE 8138250  
PUBMED  
COMMENT Submitted (06-JUN-1993) to DDBJ by:  
Hiroaki Okamoto  
Immunology Division  
Jichi Medical School  
Kawachi-gun  
Tochigi-ken 329-04  
Japan  
Phone: 0285-44-2111 x3334  
Fax: 0285-44-1557.  
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## ORIGIN

Query Match 56.4%; Score 252.2; DB 14; Length 1505;  
Best Local Similarity 72.9%; Pred. No. 9.3e-57;  
Matches 333; Conservative 1; Mismatches 119; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTGGCAACAGGAAATTTAAGTTGCTCTTTCTATCTTCTCTG 60  
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QY 241 ATCTTCACATTAAGTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
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QY 421 ACTGTCCAGACATGCAACTGCTC 443  
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RESULT 13  
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LOCUS HPCHCV048 867 bp RNA linear VRL 15-FEB-2003  
DEFINITION Hepatitis C virus DNA, clone: BA-1.  
ACCESSION D16736  
VERSION D16736.1 GI:506254  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
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Hepacivirus.

REFERENCE 1  
AUTHORS Ohno, T.  
TITLE Hepatitis C virus  
JOURNAL Thesis (1993) The University of Tokyo  
REFERENCE 2 (bases 1 to 867)  
AUTHORS Ohno, T.  
TITLE Direct Submision  
JOURNAL Submitted (08-JUL-1993) Tomoyoshi Ohno, Nagoya City University  
Medical School, Second Department of Internal Medicine, 1-1  
Kawasumi, Mizuno, Nagoya, Aichi 467, Japan  
(Tel:052-851-5511 (ex. 8748, 2265), Fax:052-852-0849)  
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Best Local Similarity 71.7%; Pred. No. 1.1e-54;  
Matches 320; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTGGCAACAGGAAATTTAAGTTGCTCTTTCTATCTTCTCTG 60  
DB 365 GACGGAATTAATTTGGCAACAGGAAATTTAAGTTGCTCTTTCTATCTTCTCTG 424  
QY 61 GCTTTGTTCTAAGCTTGTCTTACACCAACAGCCGGCTGAGTACCGTATGCTCCGA 120  
DB 425 GCTTTGTTCTAAGCTTGTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 484  
QY 121 CTCTACATGTAATTAACAGTACAGTAAAGTATGATGAGCCGGGATATT 180  
DB 485 CTCTACATGTAATTAACAGTACAGTAAAGTATGATGAGCCGGGATATT 544  
QY 181 ATCTTCACATTAAGTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
DB 545 ATCTTCACATTAAGTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 604  
QY 241 ATCTTCACATTAAGTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
DB 605 ACAGCATGTAATTAAGTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 664  
QY 301 ACAGCATGTAATTAAGTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
DB 665 ACAGCATGTAATTAAGTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 724  
QY 361 CTTTGTGAGGCGCTATTTCTTGTGGGACAGGGGTTCTCATGAGACATGCGACATTGG 420  
DB 725 CTTTGTGAGGCGCTATTTCTTGTGGGACAGGGGTTCTCATGAGACATGCGACATTGG 420  
QY 421 ACTGTCCAGACATGCAACTGCTC 446  
DB 785 ACAGTCCAGACATGCAACTGCTC 810

RESULT 14  
HPCHNB137E 1504 bp RNA linear VRL 10-JUN-1999

LOCUS HPCHNB137E 1504 bp RNA linear VRL 10-JUN-1999  
DEFINITION Hepatitis C virus RNA for core, env, and part of E2/NS1 polypeptide.  
ACCESSION D16616  
VERSION D16616.1 GI:475870  
KEYWORDS E2/NS1; core protein; envelope protein.  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Hepatitis C virus, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases)  
AUTHORS Shrestha, S.M., Tauda, F., Okamoto, H., Tokita, H., Horikita, M.,  
Tanaka, T., Miyakawa, Y., and Mayumi, M.  
TITLE Hepatitis B virus subtypes and hepatitis C virus genotypes in  
patients with chronic liver disease in Nepal  
JOURNAL Hepatology 19 (4), 805-809 (1994)  
REFERENCE 2 (bases)  
AUTHORS Tokita, H., Shrestha, S.M., Okamoto, H., Sakamoto, M., Horikita, M.,  
Iizuka, H., Shrestha, S., Miyakawa, Y., and Mayumi, M.  
TITLE Hepatitis C virus variants from Nepal with novel genotypes and  
their classification into the third major group  
JOURNAL J. Gen. Virol. 75 (Pt 4), 931-936 (1994)  
MEDLINE 94201770  
PUBMED 8138250

REFERENCE 2 (bases)  
AUTHORS Tokita, H., Shrestha, S.M., Okamoto, H., Sakamoto, M., Horikita, M.,  
Iizuka, H., Shrestha, S., Miyakawa, Y., and Mayumi, M.  
TITLE Hepatitis C virus variants from Nepal with novel genotypes and  
their classification into the third major group  
JOURNAL J. Gen. Virol. 75 (Pt 4), 931-936 (1994)  
MEDLINE 94201770  
PUBMED 8138250

COMMENT Submitted (06-JUL-1993) to DDBJ by:  
Hiroaki Okamoto  
Immunology Division  
Jichi Medical School  
Kawachi-gun

Tochigi-ken 329-04  
Japan  
Phone: 0285-44-2111 x3334  
Fax: 0285-44-1557.

## FEATURES

source

Location/Qualifiers

1..1504  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="NE137"  
/db\_xref="taxon:11103"  
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/evidence=not\_experimental  
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/codon\_start=1  
/evidence=not\_experimental  
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/protein\_id="BA04038.1"  
/db\_xref="GI:475871"

CDS

5'UTR

1 GACGGAATTAATTGGCAACAGGGAATTAACCGTGTGCTCTTCTCTATCTTCTCTG 60  
737 GACGGAATTAATTGGCAACAGGGAATTAACCGTGTGCTCTTCTCTATCTTCTCTG 796  
61 GCTTGTCTCATGCTTGTCTTACACCCAGCCGCGGCTGAGTACCGTAATGCTCCGGA 120  
797 GCTTGTCTCTCGCTTGAAGTCCCGGCGTGTGCTGAGTACAGAAACAGTCTGCG 856  
121 CTCTACATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180  
857 CTCTACATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 916  
181 ATCTCTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240  
917 ATCTCTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 976  
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977 ATCTCTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1036  
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1037 ATCTCTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1096  
361 ATCTCTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420  
1097 ATCTCTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480  
421 ATCTCTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 446  
1157 ATCTCTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1182

## ORIGIN

Query Match 54.0%; Score 241.2; DB 14; Length 1504;  
Best Local Similarity 71.3%; Pred. No. 8.3e-54;  
Matches 318; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

RESULT 15  
HPCOREIS 447 bp ss-RNA linear VRL 16-OCT-2001  
LOCUS Hepatitis C virus type 3a clone NL26 precursor protein gene,  
DEFINITION partial cds.  
ACCESSION U39298.1  
VERSION U39298.1  
KEYWORDS GI:845459

## SOURCE

ORGANISM

Hepatitis C virus type 3a  
Hepatitis C virus type 3a  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepatitis virus.

## REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

AUTHORS

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MEDLINE

Db 361 ATGTGTGGGGCCGCTCTTCCTGTGTGGACAAGCCTTCACATTCAAGCCTCGTGGCATCAA 420  
OY 421 ACTGTCCAGAGACTGTCAACTGTTC 443  
Db 421 ACGGTCCAGACTGTGTAAGTCTC 443

Search completed: December 29, 2004, 15:21:53  
Job time : 2268 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: December 29, 2004, 13:30:54 ; Search time 355 Seconds  
(without alignments)  
6609.834 Million cell updates/sec

Title: US-09-851-138c-51

Perfect score: 447  
Sequence: 1 gacgcgaatcaatttcgcaac.....aggactgcgaactgttcacac 447

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 segs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_23sep04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445.8	99.7	447	2	AAT27962
2	236.2	52.8	540	2	AAQ78031
3	236.2	52.8	541	2	AAQ78029
4	234.6	52.5	541	2	AAQ78033
5	234.6	52.5	541	2	AAQ78036
6	234.6	52.5	541	2	AAQ78032
7	233	52.1	541	2	AAQ78030
8	233	52.1	541	2	AAQ78034
9	233	52.1	541	2	AAQ78035
10	233	52.1	630	2	AAT12965
11	233	52.1	630	2	AAT12965
12	233	52.1	630	2	AAT12965
13	233	52.1	630	2	AAT12965
14	221.4	49.5	1249	2	AAQ78031
15	219.4	48.6	579	2	AAQ78034
16	217.4	48.3	579	2	AAQ78034
17	216.2	48.4	580	2	AAQ78034
18	215.8	48.3	579	2	AAQ78034
19	215.8	48.3	579	2	AAQ78034
20	215.8	48.3	579	2	AAQ78034
21	209.8	46.9	447	2	AAT27956

22	209	46.8	447	2	AAT27952	AAT27952 Hepatitis
23	208.6	46.7	447	2	AAT27955	AAT27955 Hepatitis
24	206.6	46.2	579	2	AAQ78102	AAQ78102 Hepatitis
25	206.2	46.1	579	2	AAQ78109	AAQ78109 Hepatitis
26	205	45.9	579	2	AAQ78101	AAQ78101 Hepatitis
27	204.6	45.8	579	2	AAQ78080	AAQ78080 Hepatitis
28	204.2	45.7	1270	2	AAV60668	AAV60668 Fragment
29	204.2	45.7	1562	2	AAV60672	AAV60672 Fragment
30	204.2	45.7	1553	8	AAV55222	AAV55222 plasmid P
31	204.2	45.7	2116	2	AAQ12242	AAQ12242 Encodes P
32	204.2	45.7	2829	2	AAV60673	AAV60673 Fragment
33	203	45.4	579	2	AAQ78114	AAQ78114 Hepatitis
34	203	45.4	579	2	AAQ78108	AAQ78108 Hepatitis
35	201.4	45.1	579	2	AAQ78113	AAQ78113 Hepatitis
36	201.4	45.1	579	2	AAQ78093	AAQ78093 Hepatitis
37	201	45.0	447	2	AAT27951	AAT27951 Hepatitis
38	199.4	44.6	673	2	AAV42305	AAV42305 HCV core
39	199.4	44.6	742	2	AAQ20926	AAQ20926 C10-E15 D
40	199.4	44.6	932	2	AAQ20923	AAQ20923 C10-E12 D
41	198.2	44.3	447	2	AAT27954	AAT27954 Hepatitis
42	197.8	44.3	447	2	AAT27953	AAT27953 Hepatitis
43	196.2	43.9	577	2	AAQ35082	AAQ35082 HCV env
44	196.2	43.9	633	2	AAT12706	AAT12706 HCV E1 co
45	196.2	43.9	633	6	AAI48915	AAI48915 Hepatitis

#### ALIGNMENTS

RESULT 1	
AAT27962	
ID AAT27962 standard; DNA; 447 BP.	
XX	
AC AAT27962;	
XX	
DT 11-MAR-1997 (first entry)	
XX	
DE Hepatitis C virus type 10a isolate NB98 bases 478-925.	
XX	
KW Hepatitis C virus; subtype; polymerase chain reaction; amplification;	
KW PCR; primer; probe; antibody; infection; ss.	
XX	
OS Hepatitis C virus.	
XX	
PN W09613590-A2.	
XX	
PD 09-MAY-1996.	
XX	
PF 23-OCT-1995; 95WO-EP004155.	
XX	
PR 21-OCT-1994; 94EP-00870166.	
PR 28-JUN-1995; 95EP-00870076.	
XX	
PA (INNO-) INNOGENETICS NV.	
XX	
PI Maertens G, Stuyver L;	
DR WPI; 1996-251460/25.	
DR P-PSDB; AAR6551.	
XX	
PT Hepatitis C virus poly:nucleic acid unique to unidentified sub: type -	
PT used to develop probes and primers for new sub: types and vaccines to	
PT prevent and treat infection.	
XX	
XX Claim 6; Fig 3; 150p; English.	
XX	
CC The sequences AAT27937-T27989 represent novel sequences isolated from	
CC hepatitis C virus subtypes different from subtypes 1a-c, 2a-d, 3a-f, 4a-	
CC 1, 5a and 6a. They esp. from the novel subtypes 1d-f, 2e-1, 2k, 2l, 3g,	
CC 4k-m, 7a-c or types 9, 10 or 11. The sequences corresp. to the 5'	
CC untranslated region (UR), the Core/E1, NS4 or NS5B regions of the genome.	
CC This sequence represents nucleotides 478-925 from the HCV type 10a	
CC isolate NB98. The new HCV types were isolated from patients with chronic	

CC HCV from the Benelux countries, France, Cameroon and Vietnam, because of  
CC their aberrant activities. The RNA was extracted, cDNA synthesised and  
CC PCR amplified, cloned and genotyped. The 5'UTR, Core/E1 and NS5B regions  
CC were sequenced either directly or partially and used to classify the new  
CC viruses into (sub)types based on comparison with known sequences. The  
CC sequences were used to generate the peptides AAR6424-R96524. The  
CC sequences can also be used to synthesise probes and primers for the  
CC detection of HCV in a sample. The polypeptides can be used to detect anti  
CC -HCV antibodies, for HCV typing or to prevent HCV infections  
XX  
SQ Sequence 447 BP; 82 A; 130 C; 114 G; 118 T; 0 U; 3 Other;  
Query Match 99.7%; Score 445.8; DB 2; Length 447;  
Best Local Similarity 100.0%; Pred. No. 1.4e-129;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GACGGAATTAATTTCCGCAACAGGGAATTTAATCTGTTGCTCTTCTCTATCTTCTCTG 60  
DB 1 GACGGAATTAATTTCCGCAACAGGGAATTTAATCTGTTGCTCTTCTCTATCTTCTCTG 60  
QY 61 GCTTTGTTCTCATGCTTGTGCTTACACCCAGAGCCGGGCTGAGTACCGTATGCTCCGGA 120  
DB 61 GCTTTGTTCTCATGCTTGTGCTTACACCCAGAGCCGGGCTGAGTACCGTATGCTCCGGA 120  
QY 121 CTCTACATGTAATCAACAGCTGCAAGTAAAGGATGATGATGAGCCGGGATATT 180  
DB 121 CTCTACATGTAATCAACAGCTGCAAGTAAAGGATGATGATGAGCCGGGATATT 180  
QY 181 ATCTTCACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
DB 181 ATCTTCACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
QY 241 ATCCCTGAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
DB 241 ATCCCTGAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
QY 301 ACGCAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
DB 301 ACGCAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
QY 361 CTTTGTGAGAGCGCTATTTCTTGTGAGGAGGGTCTCATGAGACATGCGCAGATTGG 420  
DB 361 CTTTGTGAGAGCGCTATTTCTTGTGAGGAGGGTCTCATGAGACATGCGCAGATTGG 420  
QY 421 ACTGTCAGAGCTGCAACTGTTCCATC 447  
DB 421 ACTGTCAGAGCTGCAACTGTTCCATC 447  
RESULT 2  
AAQ78031  
ID AAQ78031 standard; cDNA; 540 BP.  
XX  
AC AAQ78031;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-JUL-1995 (first entry)  
XX  
DE Hepatitis C virus Core/E1 region.  
XX  
KW Hepatitis C virus; HCV; primer; probe; detection; diagnosis;  
KW classification; immunisation; prophylaxis; serotyping; ss.  
XX  
OS Hepatitis C virus type 3a.  
XX  
FH Key Location/Qualifiers  
FT CDS 2..541  
FT /tag= a  
FT /product= "Core/E1 polypeptide."  
XX  
PN MO9425601-A2.  
XX  
PD 10-NOV-1994.

XX  
PF 27-APR-1994; 94MO-BP001323.  
XX  
PR 27-APR-1993; 93EP-00401099.  
PR 05-AUG-1993; 93EP-00402019.  
XX  
PA (INNO-) INNOGENETICS NV SA.  
XX  
PI Maertens G, Stuyver L;  
XX  
DR WPI; 1994-358277/44.  
DR P-PSDB; AAR63279.  
XX  
PT New polynucleotide sequences from hepatitis C virus - and related  
PT vectors, polypeptide(s) and antibodies, useful for immunisation,  
PT treatment, diagnosis and typing of HCV isolates.  
XX  
PS Claim 2; Page 107-108; 404pp; English.  
XX  
CC Compositions comprising at least 5, and pref. 8 or more contiguous  
CC nucleotides selected from an HCV type 3 genomic sequence, more  
CC particularly (i) the region spanning positions 417-957 of the Core/E1  
CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of  
CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-  
CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning  
CC positions 8023-8235 of the NS5 region of the BR5 subgroup of HCV subtype  
CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to  
CC amplify nucleic acid from an isolate belonging to a specific genotype, or  
CC as a probe for specific detection/classification of nucleic acid.  
CC Polypeptides encoded by the nucleotides in such compositions may be used  
CC for immunisation against HCV, for the detection of antibodies directed  
CC against HCV and for serotyping. This sequence corresponds to the Core/E1  
CC region of HCV subtype 3a and is taken from a clone designated HD10-2-21.  
XX  
SQ Sequence 540 BP; 105 A; 153 C; 144 G; 138 T; 0 U; 0 Other;  
Query Match 52.8%; Score 236.2; DB 2; Length 540;  
Best Local Similarity 70.7%; Pred. No. 1.1e-63;  
Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps 0;  
QY 1 GACGGAATTAATTTGCAACAGGGAATTTAATCTGTTGCTCTTCTCTATCTTCTCTG 60  
DB 61 GACGGAATTAATTTGCAACAGGGAATTTAATCTGTTGCTCTTCTCTATCTTCTCTG 120  
QY 61 GCTTTGTTCTCATGCTTGTGCTTACACCCAGAGCCGGGCTGAGTACCGTATGCTCCGGA 120  
DB 121 GCTTTGTTCTCATGCTTGTGCTTACACCCAGAGCCGGGCTGAGTACCGTATGCTCCGGA 180  
QY 121 CTCTACATGTAATCAACAGCTGCAAGTAAAGGATGATGATGAGCCGGGATATT 180  
DB 121 CTCTACATGTAATCAACAGCTGCAAGTAAAGGATGATGATGAGCCGGGATATT 240  
QY 181 ATCTTCACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
DB 181 ATCTTCACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
QY 241 ATTCTGACACACCCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
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QY 241 ATCCCTGAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
DB 301 ACCCGAGTACACCTGAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGC 360  
QY 301 ACGCAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
DB 361 AGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
QY 361 CTTTGTGAGAGCGCTATTTCTTGTGAGGAGGGTCTCATGAGACATGCGCAGATTGG 420  
DB 421 ATGTGTGAGAGCGCTATTTCTTGTGAGGAGGGTCTCATGAGACATGCGCAGATTGA 480  
QY 421 ACTGTCAGAGCTGCAACTGTTCC 443  
DB 481 ACGTCAGAGCTGCAACTGTTCC 503

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RESULT 3
AA078029 standard; cDNA, 541 BP.
ID AA078029 standard; cDNA, 541 BP.
AC
XX
XX
AA078029;
XX
XX
25-MAR-2003 (revised)
DT 20-UTL-1995 (first entry)
XX
XX
Hepatitis C virus Core/E1 region.
DE
XX
XX
Hepatitis C virus; HCV; primer: probe; detection; diagnosis;
KM classification; immunisation; prophylaxis; serotyping; ss.
XX
XX
Hepatitis C virus type 3a.
OS
XX
XX
Key Location/Qualifiers
FH 2..541
FT CDS /tag= a
FT /product= "Core/E1 polypeptide."
FT
XX
XX
MO9425601-A2.
XX
XX
10-NOV-1994.
XX
XX
27-APR-1994; 94MO-BP001323.
XX
XX
27-APR-1993; 93BP-00401099.
PR 05-AUG-1993; 93BP-00402019.
XX
XX
(INNO-) INNOGENETICS NV SA.
PA
XX
XX
Maertens G, Stuyver L;
PI
XX
XX
WPI; 1994-358277/44.
DR P-PSDB; AAR63277.
XX
XX
New polynucleotide sequences from hepatitis C virus - and related
PT vectors, polypeptide(s) and antibodies, useful for immunisation,
PT treatment, diagnosis and typing of HCV isolates.
XX
XX
Claim 2; Page 103-104; 404pp; English.
XX
XX
Compositions comprising at least 5, and pref. 8 or more contiguous
CC nucleotides selected from an HCV type 3 genomic sequence, more
CC particularly (i) the region spanning positions 417-957 of the Core/E1
CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of
CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-
CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning
CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype
CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to
CC amplify nucleic acid from an isolate belonging to a specific genotype, or
CC as a probe for specific detection/classification of nucleic acid.
CC Polypeptides encoded by the nucleotides in such compositions may be used
CC for immunisation against HCV, for the detection of antibodies directed
CC against HCV and for serotyping. This sequence corresponds to the Core/E1
CC region of HCV subtype 3a and is taken from a clone designated HD10-2-5.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
Sequence 541 BP; 104 A; 153 C; 145 G; 139 T; 0 U; 0 Other;
SO
XX
Query Match 52.8%; Score 236.2; DB 2; Length 541;
Best Local Similarity 70.7%; Pred. No. 1.1e-63;
Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps 0;
XX
OY 1 GACGGAATTATTAATTCGACAGGAAATTTACCTGCTGCTTCTATCTTCCTTCG 60
DB 62 GACGGATTAATTCGACAGGAAATTTCCCGTCTCTTCTATCTTCCTTCCTTC 121
OY 61 GCTTTGTTTCATGCTTGTACACCCACAGCCGGCTGGAGTACGTTATGCTCCGGA 120
DB 122 GCTCTGTTCTTCTTATTCATCCAGCAGCTAGTCTAGAGTGGGGAACAGCTCGGC 181
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121 CTTTACATGTAATTAACAGCTGACGTAAACGTAAGTATGCTGTATGAGCCGGGATATT 180
DB 182 CTTTATGTCCTTAACCAAGACTGTTCCAATTAATGATGATGAGGCCATGACGTT 241
OY 181 ATCTCCACTTACCTGGCTGTGTCCCTGCTACGCTTGACAAATCATCAAGATCTGG 240
DB 242 ATTCTGACACACCCGGCTGTGTACCTTGTGTTACAGAGCGTAAATCATCTGGTCTGG 301
OY 241 ATCCCTGTAGCCCTTAACCGTCCGCTGAAGTGCCTCTGCGCCGACCCGCTCTCTCCG 300
DB 302 ACCCCAGTACACCTTACAGTGGCAGTACAGTACGTGAGCAACACCCGCTTCAATACCC 361
OY 301 ACCGACGTGATATGATGTGTGGGCGGACCACTATGCTCAGCTCTTACAGTAGAGAC 360
DB 362 AGGATGTAGACATGTGTGGGCGGCGCACGATGTCTCTTCTTACGTGGGTAT 421
OY 361 CTTTGTGAGCCCTATTTCTTGTGGGCGAGGGATTCTCATGAGCATGCCAGATTGG 420
DB 422 ATGTGTGGGCGCGTCTTCTCGTGGGACAAAGCCTTCAAGCTGTGCGCATCA 481
OY 421 ACTGTCCAGACTGCAACTGTTC 443
DB 482 ACGTCCAGACCTGTAACTGCTC 504
XX
XX
RESULT 4
AA078033
ID AA078033 standard; cDNA, 541 BP.
XX
XX
AA078033;
XX
XX
25-MAR-2003 (revised)
DT 01-AUG-1995 (first entry)
XX
XX
Hepatitis C virus Core/E1 region.
DE
XX
XX
Hepatitis C virus; HCV; primer: probe; detection; diagnosis;
KM classification; immunisation; prophylaxis; serotyping; ss.
XX
XX
Hepatitis C virus type 3a.
XX
XX
Key Location/Qualifiers
FH 2..541
FT CDS /tag= a
FT /product= "Core/E1 polypeptide."
FT
XX
XX
MO9425601-A2.
XX
XX
10-NOV-1994.
XX
XX
27-APR-1994; 94MO-BP001323.
XX
XX
27-APR-1993; 93BP-00401099.
PR 05-AUG-1993; 93BP-00402019.
XX
XX
(INNO-) INNOGENETICS NV SA.
PA
XX
XX
Maertens G, Stuyver L;
PI
XX
XX
WPI; 1994-358277/44.
DR P-PSDB; AAR63281.
XX
XX
New polynucleotide sequences from hepatitis C virus - and related
PT vectors, polypeptide(s) and antibodies, useful for immunisation,
PT treatment, diagnosis and typing of HCV isolates.
XX
XX
Claim 2; Page 111-112; 404pp; English.
XX
XX
Compositions comprising at least 5, and pref. 8 or more contiguous
CC nucleotides selected from an HCV type 3 genomic sequence, more
CC particularly (i) the region spanning positions 417-957 of the Core/E1
CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of
```



CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-  
 CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning  
 CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype  
 CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to  
 CC amplify nucleic acid from an isolate belonging to a specific genotype, or  
 CC as a probe for specific detection/classification of nucleic acid.  
 CC Polypeptides encoded by the nucleotides in such compositions may be used  
 CC for immunisation against HCV, for the detection of antibodies directed  
 CC against HCV and for serotyping. This sequence corresponds to the Core/E1  
 CC region of HCV subtype 3a and is taken from a clone designated BR36-9-20.  
 CC (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 541 BP; 106 A; 154 C; 142 G; 139 T; 0 U; 0 Other;

Query Match 52.5%; Score 234.6; DB 2; Length 541;

Best Local Similarity 70.4%; Pred. No. 3.6e-63; Mismatches 130; Indels 0; Gaps 0;

Matches 312; Conservative 1; Mismatches 130; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGCAACAGGAAATTTACCTGTGCTCTTCTCTATCTTCTCTG 60  
 DB 62 GACGGGATTAATTTCGCAACAGGAAATTTGCGGTGCTCTTCTATTTTCTCTT 121

QY 61 GCTTTGTTCTCATGCTTCTCTTACACCAACAGCGGCTGGAGTACCGTATGCTCCGA 120  
 DB 122 GCTGTGTTCTCTTCTTAAATTCATCCAGAGCTAGTCTAGAGTGGCGGAATACGTCTGC 181

QY 121 CTCTACATGTAATTAACAGACTCAGTAACGAGTATGCTGATAGAGCCGGGATAT 180  
 DB 182 CTCTATGCTCTTACCAACAGCTCTTCCATAGACAGTATGTTGACAGGCGCATGACGTT 241

QY 181 ATCTCTCACTTACCTGCTGTGTCCCTGCGTACGCTCTGCGAATACATCAAGACTG 240  
 DB 242 ATTCTGCAACACCCGCTGTATACCTTGTGTCAGAGCGGCAATATCAAGTCTCG 301

QY 241 ATCCCTGAGACCCCTACCGTCCGCTGGAAGTGCCTCTGGCGGCCACCGCTCTCTCG 300  
 DB 302 ACCCGAGTACACTACAGTGCAGTCAAGTACGTGAGCAACACCGCTCTGATACGC 361

QY 301 ACGCAGTGAATATGATGTGGGCGGCCACCCATAGCTAGCTCTTACGTAAGAGAC 360  
 DB 362 AGTCATGTGAGCACTTATTAAGTGGCGCGGCCACGATGCTCTGCTTACGTTGAGTGC 421

QY 361 CTTTGTGAGCGCTATTTCTTGTGGGCGAGGGTCTCTCATGAGACATCGCCAGCAT 420  
 DB 422 ATGTGTGGGCGTGTCTTCTCGTGGGACAAGCCTTACGTTGAGACCTGCTGATCA 481

QY 421 ACTGTCCAGACTGCAACTGTTTC 443  
 DB 482 ACGGTCCAGACTGTAACGTGCTC 504

RESULT 5

AAQ78036 standard; cDNA; 541 BP.

AC AAQ78036;  
 XX  
 AC  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 01-AUG-1995 (first entry)  
 XX  
 DE Hepatitis C virus Core/E1 region.  
 XX  
 KM Hepatitis C virus; HCV; primer; probe; detection; diagnosis;  
 KM classification; immunisation; prophylaxis; serotyping; ss.  
 XX  
 OS Hepatitis C virus type 3a.  
 XX  
 FX  
 FX Key Location/Qualifiers  
 FH 2.541  
 FT /tag= a  
 FT /product= "Core/E1 polypeptide."  
 XX  
 FN

W09425601-A2.

XX 10-NOV-1994.  
 PD 94MO-EP001323.  
 XX  
 PF 27-APR-1994;  
 XX  
 PR 27-APR-1993; 93EP-00401099.  
 PR 05-AUG-1993; 93EP-00402019.  
 XX  
 PA (INNO-) INNOGENETICS NV SA.  
 XX  
 PI Maertens G, Stuyver L;  
 XX  
 DR WPI; 1994-358277/44.  
 DR P-PSDB; AAR63284.  
 XX  
 PT New polynucleotide sequences from hepatitis C virus - and related  
 PT vectors, polypeptide(s) and antibodies, useful for immunisation,  
 PT treatment, diagnosis and typing of HCV isolates.  
 XX  
 PS Claim 2; Page 117-118; 404pp; English.

CC Compositions comprising at least 5, and pref. 8 or more contiguous  
 CC nucleotides selected from an HCV type 3 genomic sequence, more  
 CC particularly (i) the region spanning positions 417-957 of the Core/E1  
 CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of  
 CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-  
 CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning  
 CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype  
 CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to  
 CC amplify nucleic acid from an isolate belonging to a specific genotype, or  
 CC as a probe for specific detection/classification of nucleic acid.  
 CC Polypeptides encoded by the nucleotides in such compositions may be used  
 CC for immunisation against HCV, for the detection of antibodies directed  
 CC against HCV and for serotyping. This sequence corresponds to the Core/E1  
 CC region of HCV subtype 3a and is taken from a clone designated BR33-1-20.  
 CC (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 541 BP; 100 A; 154 C; 148 G; 139 T; 0 U; 0 Other;

Query Match 52.5%; Score 234.6; DB 2; Length 541;

Best Local Similarity 70.4%; Pred. No. 3.6e-63; Mismatches 130; Indels 0; Gaps 0;

Matches 312; Conservative 1; Mismatches 130; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGCAACAGGAAATTTACCTGTGCTCTTCTCTATCTTCTCTG 60  
 DB 62 GACGGGATTAATTTCGCAACAGGAAATTTGCGGTGCTCTTCTATTTTCTCTT 121

QY 61 GCTTTGTTCTCATGCTTCTCTTACACCAACAGCGGCTGGAGTACCGTATGCTCCGA 120  
 DB 122 GCTGTGTTCTCTTCTTAACTTCCATAGCAGCTGCTTGAAGTGGCGGAATACGTCTGC 181

QY 121 CTCTACATGTAATTAACAGACTCAGTAACGAGTATGCTGATAGAGCCGGGATAT 180  
 DB 182 CTCTATGCTCTTACCAACAGCTCTTCAATGATATGTTGATAGAGCGGATACGTT 241

QY 181 ATCTCTCACTTACCTGCTGTGTCCCTGCGTACGCTCTGCGAATACATCAAGATGCTG 240  
 DB 242 ATTCTGCAACACCCGCTGTATACCTTGTGTCAGAGCGGCAATATCAAGTCTCG 301

QY 241 ATCCCTGAGACCCCTACCGTCCGCTGGAAGTGCCTCTGGCGGCCACCGCTCTCTCG 300  
 DB 302 ACCCGAGTACACTACAGTGCAGTCAAGTACGTGCGGGAACACCGCTCTGATACGC 361

QY 301 ACGCAGTGAATATGATGTGGGCGGCCACCCATAGCTAGCTCTTACGTAAGAGAC 360  
 DB 362 AGTCATGTGAGCACTTATTAAGTGGCGGCCACGATGCTCTGCGCTTACGTTGAGTAT 421

QY 421 CTTTGTGAGCGCTATTTCTTGTGGGCGAGGGTCTCATGAGACATCGCCAGCAT 420  
 DB 422 ATGTGTGGGCGCTTCTCTGTTGGGACAAGCCTTCAAGTTCAGACCCGCGCATCA 481

QY 421 ACTGTCCAGACTGCAACTGTTTC 443

Db 482 ACGGTCCAGACTGTAACTGTTTC 504

RESULT 6  
AAQ78032  
ID AAQ78032 standard; cDNA; 541 BP.  
XX  
AC AAQ78032;  
XX  
DT 25-MAR-2003 (revised)  
DT 01-AUG-1995 (first entry)  
XX  
DE Hepatitis C virus Core/E1 region.  
XX  
KW Hepatitis C virus; HCV; primer; probe; detection; diagnosis;  
KW classification; immunisation; prophylaxis; serotyping; ss.  
XX  
OS Hepatitis C virus type 3a.

Key Location/Qualifiers  
FT CDS 2..541  
FT /tag= a  
FT /product= "Core/E1 polypeptide."

PN MO9425601-A2.  
XX  
PD 10-NOV-1994.  
XX  
PF 27-APR-1994; 94MO-EP001323.  
XX  
PR 27-APR-1993; 93EP-00401099.  
PR 05-AUG-1993; 93EP-00402019.  
XX  
PA (INNO-) INNOGENETICS NV SA.  
XX  
PI Maertens G, Stuyver L;  
XX  
DR WPI, 1994-358277/44.  
DR P-PSDB; AAR63280.

PT New polynucleotide sequences from hepatitis C virus - and related  
PT vectors, polypeptide(s) and antibodies, useful for immunisation,  
PT treatment, diagnosis and typing of HCV isolates.

PS Claim 2; Page 109-110; 404pp; English.

CC Compositions comprising at least 5, and pref. 8 or more contiguous  
CC nucleotides selected from an HCV type 3 genomic sequence, more  
CC particularly (i) the region spanning positions 417-957 of the Core/E1  
CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of  
CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-  
CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning  
CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype  
CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to  
CC amplify nucleic acid from an isolate belonging to a specific genotype, or  
CC as a probe for specific detection/classification of nucleic acid.  
CC Polypeptides encoded by the nucleotides in such compositions may be used  
CC for immunisation against HCV, for the detection of antibodies directed  
CC against HCV and for serotyping. This sequence corresponds to the Core/E1  
CC region of HCV subtype 3a and is taken from a clone designated BR36-9-13.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX  
SQ Sequence 541 BP; 107 A; 155 C; 142 G; 137 T; 0 U; 0 Other;

Query Match 52.5%; Score 234.6; DB 2; Length 541;  
Best Local Similarity 70.4%; Pred. No. 3, 6e-63;  
Matches 312; Conservative 1; Mismatches 130; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTGGCAACAGGAAATTAACGTTGCTCTTCTCTATCTTCTTCTG 60  
DB 62 GACGGATTAATTTCCGCAACAGGAAATTTGCCGTTGCTCTTCTATTTCTTCTT 121  
QY 61 GCTTTGTTCTCAAGCTTGTCTTACACCAACGCGGCTGGAGTACCGTATGCTCCGA 120

Db 122 GCTCTGTTCTTCTGCTTAATTCATCCAGACGCTAGCTAGTGGCGGAATACGTCTCCG 181  
QY 121 CTCTACATGTATTAACACGCTGCACTGAACGAGTATGATGATGAGCCGGGATATT 180  
DB 182 CTCTATGTCCTTACCAAGACGCTGTTCCAAATAGACGATATTGTGACGAGCGCATGACGTT 241  
QY 181 ATCTTCCACTTACCTGCTGTGTGCTCCCTGCGTACGCTCTGGCAATACATCAAGATGCTGG 240  
DB 242 ATTTCGACACACCCGCGTGCATACCTTGTGTCCAGAGACGAAATTCATCCAGTCTCG 301  
QY 241 ATCCCTGTAGAGCCVYACCGTGGCCGTGAAGTGCCCTGCGCGCCACGCTCTCTCCG 300  
DB 302 ACCCGATACACCTTCAAGTGGAGTCAAGTACGTTGAGCAACACCGCTTGATACCG 361  
QY 301 ACGCAGTGAATATGATGTGGGCGGCAACCTATGCTCACTGCTTCACTGATGAGAC 360  
DB 362 AGTCATGTGGACCTATTATGTGGGCGGCGCAAGATGTGCTACGCGCTTACGTTGATGAT 421  
QY 361 CTTTGTGAGCGCTATTCTTGTGGGCGAGGGTTCTCATGAGACATGCGCAGATTGG 420  
DB 422 ATGTGTGGGCGCGTCTTCTTGTGGGCAAGCCTTCACTGACCTGCTGCTCATCA 481  
QY 421 ACTGTCCAGACTGCAACTGTTTC 443  
DB 482 ACGGTCCAGACTGTAACTGTTTC 504

RESULT 7  
AAQ78030  
ID AAQ78030 standard; cDNA; 541 BP.  
XX  
AC AAQ78030;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-JUL-1995 (first entry)  
XX  
DE Hepatitis C virus Core/E1 region.  
XX  
KW Hepatitis C virus; HCV; primer; probe; detection; diagnosis;  
KW classification; immunisation; prophylaxis; serotyping; ss.  
XX  
OS Hepatitis C virus type 3a.

PS Claim 2; Page 105-106; 404pp; English.

CC Compositions comprising at least 5, and pref. 8 or more contiguous  
CC nucleotides selected from an HCV type 3 genomic sequence, more

Key Location/Qualifiers  
FT CDS 2..541  
FT /tag= a  
FT /product= "Core/E1 polypeptide."

PN MO9425601-A2.  
XX  
PD 10-NOV-1994.  
XX  
PF 27-APR-1994; 94MO-EP001323.  
XX  
PR 27-APR-1993; 93EP-00401099.  
PR 05-AUG-1993; 93EP-00402019.  
XX  
PA (INNO-) INNOGENETICS NV SA.  
XX  
PI Maertens G, Stuyver L;  
XX  
DR WPI, 1994-358277/44.  
DR P-PSDB; AAR63278.

PT New polynucleotide sequences from hepatitis C virus - and related  
PT vectors, polypeptide(s) and antibodies, useful for immunisation,  
PT treatment, diagnosis and typing of HCV isolates.

CC particularly (i) the region spanning positions 417-957 of the Core/E1  
CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of  
CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-  
CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning  
CC positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype  
CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to  
CC amplify nucleic acid from an isolate belonging to a specific genotype, or  
CC as a probe for specific detection/classification of nucleic acid.  
CC Polypeptides encoded by the nucleotides in such compositions may be used  
CC for immunisation against HCV, for the detection of antibodies directed  
CC against HCV and for serotyping. This sequence corresponds to the Core/E1  
CC region of HCV subtype 3a and is taken from a clone designated HD10-2-14.  
CC (updated on 25-MAR-2003 to correct PN field.)

XX Sequence 541 BP; 106 A; 154 C; 143 G; 138 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 2; Length 541;  
Best Local Similarity 70.2%; Pred. No. 1.1e-62;  
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAAATTAATTTGGCAAGGGAATTAACCTGGTCTCTTCTATCTTCTCTCG 60  
DB 62 GACGGAAATTAATTTGGCAAGGGAATTAACCTGGTCTCTTCTATCTTCTCTCG 121  
QY 61 GCTTGTCTCATGCTTGTCTTACACCCAGCCGCGCTGAGTACCGTATGCTCCGA 120  
DB 122 GCTTGTCTCTTGTCTTATTCATCCAGCAGTATGCTAGTGGGGAACAGCTTGGC 181  
QY 121 CTCTACATGTAATTAACGATCAGTAAACGATGATGATGATGATGATGATGAT 180  
DB 182 CTCTATGTCCTTACCAACGATGCTTCCAAATAGCAATGATGATGATGATGATG 241  
QY 181 ATCCCTCACTTACCTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
DB 242 ATCTTCAACACACCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 301  
QY 241 ATCCCTGTGAGCCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 300  
DB 302 ACCCGAGTACACCTTACGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 361  
QY 301 AGCGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
DB 362 AGCGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 421  
QY 361 CTCTTGTGAGCGCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 420  
DB 422 ATGT 481  
QY 421 ACTGTCCAGGACTGCAACTGTTC 443  
DB 482 ACGGTCCAGACCTGTAACTGTCTC 504

RESULT 8  
AAQ78034  
ID AAQ78034 standard; cDNA; 541 BP.  
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AC AAQ78034;  
XX  
DT 25-MAR-2003 (revised)  
DT 01-AUG-1995 (first entry)  
XX  
DE Hepatitis C virus Core/E1 region.  
XX  
XX Hepatitis C virus; HCV; primer, probe, detection; diagnosis;  
KM classification; immunisation; prophylaxis; serotyping; ss.  
XX  
OS Hepatitis C virus type 3a.

FH Key Location/Qualifiers  
FT CDS 2..541  
FT /tag= a  
FT /product= "Core/E1 polypeptide."

XX  
PN WO9425601-A2.  
XX  
PD 10-NOV-1994.  
XX  
PF 27-APR-1994; 94WO-BP001323.  
XX  
PR 27-APR-1993; 93EP-00401099.  
PR 05-AUG-1993; 93EP-00402019.  
XX  
PA (INNO-) INNOGENETICS NV SA.  
XX  
PI Maertens G, Stuyver L;  
XX  
DR WPI; 1994-358277/44.  
XX  
DR P-PsDB; AAR63282.  
XX  
PT New polynucleotide sequences from hepatitis C virus - and related  
PT vectors, polypeptide(s) and antibodies, useful for immunisation,  
PT treatment, diagnosis and typing of HCV isolates.  
XX  
PS Claim 2, Page 113-114, 404pp; English.

XX Compositions comprising at least 5, and pref. 8 or more contiguous  
XX nucleotides selected from an HCV type 3 genomic sequence, more  
XX particularly (i) the region spanning positions 417-957 of the Core/E1  
XX region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of  
XX the NS3 region of HCV type 3; (iii) the region spanning positions 4892-  
XX 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning  
XX positions 8023-8235 of the NS5 region of the BR36 subgroup of HCV subtype  
XX 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to  
XX amplify nucleic acid from an isolate belonging to a specific genotype, or  
XX as a probe for specific detection/classification of nucleic acid.  
XX Polypeptides encoded by the nucleotides in such compositions may be used  
XX for immunisation against HCV, for the detection of antibodies directed  
XX against HCV and for serotyping. This sequence corresponds to the Core/E1  
XX region of HCV subtype 3a and is taken from a clone designated BR33-1-10.  
XX (Updated on 25-MAR-2003 to correct PN field.)

SO Sequence 541 BP; 100 A; 157 C; 148 G; 136 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 2; Length 541;  
Best Local Similarity 70.2%; Pred. No. 1.1e-62;  
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAAATTAATTTGGCAAGGGAATTAACCTGGTCTCTTCTATCTTCTCTCG 60  
DB 62 GACGGAAATTAATTTGGCAAGGGAATTAACCTGGTCTCTTCTATCTTCTCTCG 121  
QY 61 GCTTGTCTCATGCTTGTCTTACACCCAGCCGCGCTGAGTACCGTATGCTCCGA 120  
DB 122 GCTTGTCTCTTGTCTTATTCATCCAGCAGTATGCTAGTGGGGAACAGCTTGGC 181  
QY 121 CTCTACATGTAATTAACGATCAGTAAACGATGATGATGATGATGATGATGATGAT 180  
DB 182 CTCTATGTCCTTACCAACGATGCTTCCAAATAGTATGATGATGATGATGATGATG 241  
QY 181 ATCCCTCACTTACCTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
DB 242 ATCTTGTGAGCGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 301  
QY 241 ATCCCTGTGAGCCGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 300  
DB 302 ACCCGAGTACACCTTACGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 361  
QY 301 AGCGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
DB 362 AGT 421  
QY 361 CTCTTGTGAGCGCTATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 420  
DB 422 ATGT 481

OY 421 ACTGTCCAGACGTCACCTGTC 443  
 DB 482 ACGGTCCAGACCTGTAACTGCTC 504

RESULT 9  
 AAQ78035  
 ID AAQ78035 standard; cDNA; 541 BP.

XX AAQ78035;

AC 25-MAR-2003 (revised)

DT 01-AUG-1995 (first entry)

XX Hepatitis C virus Core/E1 region.

XX Hepatitis C virus; HCV; primer; probe; detection; diagnosis;  
 KM classification; immunisation; prophylaxis; serotyping; ss.

OS Hepatitis C virus type 3a.

XX Key Location/Qualifiers

FT CDS 2..541

FT /\*tag= a

PN MO9425601-A2.

PD 10-NOV-1994.

PF 27-APR-1994; 94MO-EP001323.

PR 27-APR-1993; 93EP-00401099.

PR 05-AUG-1993; 93EP-00402019.

XX (INNO-) INNOGENETICS NV SA.

XX Maertens G, Stuyver L;

XX MPI; 1994-358277/44.

XX P-PSDB; AAR63283.

PT New polynucleotide sequences from hepatitis C virus - and related  
 PT vectors, polypeptide(s) and antibodies, useful for immunisation,  
 treatment, diagnosis and typing of HCV isolates.

XX Claim 2; Page 115-116; 404pp; English.

XX Compositions comprising at least 5, and pref. 8 or more contiguous  
 CC nucleotides selected from an HCV type 3 genomic sequence, more  
 CC particularly (i) the region spanning positions 417-957 of the Core/E1  
 CC region of HCV subtype 3a; (ii) the region spanning positions 4664-4730 of  
 CC the NS3 region of HCV type 3; (iii) the region spanning positions 4892-  
 CC 5292 of the NS3/4 region of HCV type 3; (iv) the region spanning  
 CC positions 8023-8235 of the NS5 region of the BR3 subgroup of HCV subtype  
 CC 3a; or (v) an HCV subtype 3c genomic sequence, may be used as primers to  
 CC amplify nucleic acid from an isolate belonging to a specific genotype, or  
 CC as a probe for specific detection/classification of nucleic acid.  
 CC Polypeptides encoded by the nucleotides in such compositions may be used  
 CC for immunisation against HCV, for the detection of antibodies directed  
 CC against HCV and for serotyping. This sequence corresponds to the Core/E1  
 CC region of HCV subtype 3a and is taken from a clone designated BR33-1-19.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 541 BP; 100 A; 155 C; 148 G; 138 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 2; Length 541;

Best Local Similarity 70.2%; Pred. No. 1,1e-62;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

OY 1 GACGGAATTAATTCGACAGGGAATTTACTGTTGCTCTTCTATCTTCCTCTG 60  
 DB 62 GACGGATTAATTCGACAGGGAATTTGCGGTTGCTCTTCTATCTTCCTCTT 121

OY 61 GCTTTGTTCTCAGTCTGCTTACACCCAGCCGGCTGAGTACGTAATGCTCCGA 120  
 DB 122 GCTGTGTTCTCTGTCTTAATTCATCCAGCGCTGTCTAGATGGGGAATAGTCTGGC 181  
 OY 121 CTCTACATGTAATCACTACAGACGTCAGTAACGGAATGATGATGAGCCGGGATATT 180  
 DB 182 CTCTATGTCCTTAACACAGACGTCGTAATGATGATGATGAGCCGATGACGTT 241  
 OY 181 ATCTCCACTTACCTGCTGTGTCTCCCTGCGTACGCTTGGCAATACATCAAGATGCTG 240  
 DB 242 ATCTGCACGCGCGCGCTGTGTACCTTGTGTCCAGACGCGAATACGCTACATGCTGG 301  
 OY 241 ATCCCTGTGAGCCCTACCGTCCGCGGAAAGTGGCCCTGCGCCGACCCGCTCTCTCCG 300  
 DB 302 ACCCCAGTAACACCTACATGTGACGATGAGTGTGCGGGCAACACCGCTTGAATACG 361  
 OY 301 ACCGACGTGATATGATGTGAGGCGGCGACCGTATGCTCAGCTCTACGTAAGAGAC 360  
 DB 362 AGTCATGTGACCTGTATGATGAGCGCGGACGATGTGCTTACGCTTACGTGGGTGAT 421  
 OY 361 CTTTGTGAGCGCTATTTCTGTGTGGGCAAGGGTTCTCATGAGACATCGCAGATTGG 420  
 DB 422 ATGTGTGGGGCGGTCTTCTCGTGGGCAAGGCTTACGTTGAGACCCGCGCATCA 481  
 OY 421 ACTGTCCAGACGTCACCTGTC 443  
 DB 482 ACGGTCCAGACCTGTAACTGCTC 504

RESULT 10

AA112965  
 ID AA112965 standard; DNA; 630 BP.

XX AA112965;

XX 24-SEP-1996 (first entry)

XX HCV E1 construct HCC162.

XX HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human;  
 KM serotype; reversed phase hybridisation assay; genotype; antigen; sera;  
 KM ss.

XX Hepatitis C virus.

XX MO9604385-A2.

XX 15-FEB-1996.

XX 31-JUL-1995; 95MO-EP003031.

XX 29-JUL-1994; 94EP-00870132.

XX (INNO-) INNOGENETICS NV.

XX Maertens G, Bosman F, De Martynoff G, Buyse M;

XX MPI; 1996-129401/13.

PT Purifying recombinant hepatitis C virus (HCV) E1 and E2 envelope proteins  
 PT - in presence of disulphide bond cleavage agent, to produce proteins  
 PT suitable for direct use in vaccines or diagnostic assays of HCV.

XX Claim 23; Fig 21; 146pp; English.

XX AA112704-T12709 and AA112961-T12974 represent hepatitis C virus (HCV) E1  
 CC and E2 protein coding sequence constructs. These sequences are included  
 CC in vectors for the production of recombinant E1, E2, and E1/E2 proteins.  
 CC The recombinant proteins can then be isolated using a method of the  
 CC invention. In the method, the envelope proteins are purified by carrying  
 CC out a disulphide bond cleavage, or a reduction step with a disulphide  
 CC bond cleavage agent, after lysis of recombinant host cells. The

CC constructs containing the purified HCV envelope proteins can be used for  
CC vaccinating humans against HCV, for in vitro detection of HCV antibodies  
CC in a sample, and in a serotyping assay for detecting one or more  
CC serological types of HCV present in a biological sample. The constructs  
CC can also be immobilised on a solid substrate and incorporated into a  
CC reversed phase hybridisation assay for determining the presence or the  
CC genotype of HCV. The new purification method preserves the conformation  
CC of the recombinantly expressed E1, E2 and E1/E2, and eliminates  
CC contaminating proteins. Antigens isolated using this method are more  
CC reactive with human sera than those isolated by known techniques  
XX

Sequence 630 BP; 127 A; 175 C; 168 G; 160 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 2; Length 630;  
Best Local Similarity 70.2%; Pred. No. 1.2e-62;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTGGCAACAGGGAATTTACTGTTGCTCTTCTCTATCTTCTCTG 60  
DB 124 GACGGGATTAATTTCCCAACAGGGAATTTGCCGGTGTCTCTTTCTATTTCTCTTC 183  
QY 61 GCTTGTCTCAATGCTTGTCTTACCCACAGCGCGGCTGGAGTACCGTATGCTCCGGA 120  
DB 184 GCTCTGTCTCTTGTCTTAAATTCATCCAGAGCTAGTCTAGAGTGGCGAATACGTCTGC 243  
QY 121 CTCTACATGTAATTAACAGACTGACAGTAAAGTATGATGATGAGCCGGGATATT 180  
DB 244 CTCTATGTCCTTACCAACAGACTGTTCCAAATGAGATATGTGATGAGGCCATGACGT 303  
QY 181 ATCTCCACTTAATCTGCTGTGTCTCCCTGGGTAAGCTCTGGCAATACATCAAGATCTG 240  
DB 304 ATTTTCACACACACCCGGCTGCATACCTTGTCTCAGAGCGGCAATTCATCCAGTCTG 363  
QY 241 ATCCCTGTAGAGCCGTCACCGTGCAGTGAAGTGCCTGTGGCGCCACCGCTCTCCGC 300  
DB 364 ACCCAGTACACTTACAGTGCAGTCAAGTACGTGAGCAACACCGCTTGATACG 423  
QY 301 ACGCAGTGAATATGATGTGGGCGGCGCACCTTATGCTCAAGCTCTTACATGAGAGAC 360  
DB 424 AGTCATGTGAGACTTATGATGGGCGGCGCACAGATGTGCTGCGCTTACGTGGTGA 483  
QY 361 CTTTGTGAGAGCGTATTTCTTGTGGGCGAGGGTTCTCATGAGACATGCCAGCATTTG 420  
DB 484 ATGTGTGGGGCTGTCTTCTGTGGGCAAGACCTTCAAGCTTCAGACCTGTGCGCATCA 543  
QY 421 ACTGTCCAGAGACTGCAACTGTTTC 443  
DB 544 ACGGTCCAGACTGTAACTGCTC 566

RESULT 11

AAL48929  
ID AAL48929 standard; DNA; 630 BP.

XX AAL48929;

XX 24-OCT-2002 (first entry)

DE Hepatitis C virus clone HCC162 E1 protein coding sequence.

XX Hepatitis C virus; HCV; E1 protein; E2 protein; infection; gene;  
KW virulence; immunostimulant; vaccine; ds.

XX Hepatitis C virus.

XX WO20025548-A2.

XX 18-JUL-2002.

PF 11-JAN-2002; 2002WO-BP000219.

PR 11-JAN-2001; 2001US-0260669P.

PR 30-AUG-2001; 2001US-0315768P.

XX (INNO-) INNOGENETICS NV.

XX Maertens G, Bosman F, Buysse M;

XX WPI; 2002-59657/64.

DR P-PSDB; AAO18670.

PT New therapeutic vaccine compositions comprising at least one purified

PT recombinant hepatitis C virus (HCV) single or specific oligonucleic

PT recombinant envelope protein E1 or E2, useful for immunizing humans from

XX HCV infection.

Example 2; Page 181-182; 243pp; English.

CC The present invention relates to new therapeutic vaccine compositions for  
CC inducing hepatitis C virus (HCV)-specific antibodies, comprising a  
CC composition containing at least one purified recombinant HCV single or  
CC specific oligonucleic recombinant envelope proteins selected from an E1 and  
CC an E2 protein, and optionally a pharmaceutical adjuvant. The vaccines are  
CC useful for inducing HCV-specific antibodies or for immunising humans  
CC against HCV. The recombinant HCV E1 and/or E2 proteins are useful as  
CC vaccines or therapeutics, in HCV screening and confirmatory antibody  
CC tests, for raising antibodies, in the preparation of medicament, and for  
CC in vitro monitoring of HCV disease or prognosing the response to  
CC treatment of patients suffering from HCV infection. The present sequence  
CC is a coding sequence described in the exemplification of the invention

Sequence 630 BP; 127 A; 175 C; 168 G; 160 T; 0 U; 0 Other;

Query Match 52.1%; Score 233; DB 6; Length 630;  
Best Local Similarity 70.2%; Pred. No. 1.2e-62;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTGGCAACAGGGAATTTACTGTTGCTCTTCTCTATCTTCTCTG 60  
DB 124 GACGGGATTAATTTGGCAACAGGGAATTTGCCGGTGTCTCTTTCTATTTCTCTTC 183  
QY 61 GCTTGTCTCAATGCTTGTCTTACCCACAGCGGCTGGAGTACCGTATGCTCCGGA 120  
DB 184 GCTCTGTCTCTTGTCTTAAATTCATCCAGAGCTAGTCTAGAGTGGCGAATACGTCTGC 243  
QY 121 CTCTACATGTAATTAACAGACTGACAGTAAAGTATGATGATGAGCCGGGATATT 180  
DB 244 CTCTATGTCCTTACCAACAGACTGTTCCAAATGAGATATGTGATGAGGCCATGACGT 303  
QY 181 ATCTCCACTTAATCTGCTGTGTCTCCCTGGGTAAGCTCTGGCAATACATCAAGATCTG 240  
DB 304 ATTTTCACACACACCCGGCTGCATACCTTGTCTCAGAGCGGCAATTCACAGTCTG 363  
QY 241 ATCCCTGTAGAGCCGTCACCGTGCAGTGAAGTGCCTGTGGCGCCACCGCTCTCCGC 300  
DB 364 ACCCAGTACACTTACAGTGCAGTCAAGTACGTGAGCAACACCGCTTGATACG 423  
QY 301 ACGCAGTGAATATGATGTGGGCGGCGCACCTTATGCTCAAGCTCTTACATGAGAGAC 360  
DB 424 AGTCATGTGAGACTTATGATGGGCGGCGCACAGATGTGCTGCGCTTACGTGGTGA 483  
QY 361 CTTTGTGAGAGCGTATTTCTTGTGGGCGAGGGTTCTCATGAGACATGCCAGCATTTG 420  
DB 484 ATGTGTGGGGCTGTCTTCTGTGGGCAAGACCTTCAAGCTTCAGACCTGTGCGCATCA 543  
QY 421 ACTGTCCAGAGACTGCAACTGTTTC 443  
DB 544 ACGGTCCAGACTGTAACTGCTC 566

RESULT 12

ADDS5537  
ID ADDS5537 standard; DNA; 630 BP.

XX ADDS5537;

DT 15-JAN-2004 (first entry)  
 XX Hepatitis C virus E1/E2 protein coding sequence #5.  
 XX  
 DE Hepatitis C virus; HCV; vaccine; liver disease; E1 protein; E2 protein;  
 KW liver fibrosis; ds, gene.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO2003051912-A2.  
 XX  
 PD 26-JUN-2003.  
 XX  
 PF 18-DEC-2002; 2002MO-EP014480.  
 XX  
 PR 18-DEC-2001; 2001US-00020510.  
 XX  
 PR 16-OCT-2002; 2002US-0418358P.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Maertens G, Depla E, Bosman F;  
 XX  
 DR WPI; 2003-541632/51.  
 XX  
 DR P-PSDB; ADD55538.  
 XX  
 PT New hepatitis C virus (HCV) vaccine composition, useful for reducing  
 XX liver disease, e.g., liver fibrosis in a chronic HCV-infected mammal.  
 XX  
 PS Example 2; SEQ ID NO 29; 271bp; English.  
 XX  
 CC The invention comprises an Hepatitis C virus (HCV) vaccine for reducing  
 CC liver disease. The vaccine of the invention comprises an HCV E1 or E2  
 CC protein as an antigen. The HCV vaccine is useful for reducing liver  
 CC disease (e.g. liver fibrosis) in a chronic HCV-infected mammal. The  
 CC present DNA sequence encodes an HCV E1/E2 protein.  
 XX  
 SQ Sequence 630 BP; 127 A; 175 C; 168 G; 160 T; 0 U; 0 Other;  
 XX  
 Query Match 52.1%; Score 233; DB 10; Length 630;  
 Best Local Similarity 70.2%; Pred. No. 1.2e-62;  
 Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;  
 XX  
 QY 1 GAGGGAATTAATTTCCAGAGGAAATTTACCTGTTGCTTCTTCTATCTTCTCTG 60  
 DB 124 GAGGGGATTAATTTCCAGAGGAAATTTGCGGTGCTCTTCTTCTATTTCTTCTC 183  
 QY 61 GCTTGTCTCATGCTTGTGTTACCAACCAAGCCGGGCTGAGTACGTAATGCTCGGA 120  
 DB 184 GCTGTGTCTCTGCTTAATTCACAGACGCTAGTCTAGTAGTGCGGAATACGTGCGC 243  
 QY 121 CTCTACATGTAATCTAACAAGTCAAGTACGTAAGTCTGTATGAGGCGGGAATATT 180  
 DB 244 CTCTAATGCTTACCAACGACTGTTCCATATGAGCAATGTTGTACGAGGCGGATGACGTT 303  
 QY 181 ATCTCTCACTTACCTGCTGTGTCCCTGTGTACGCTCTGGAATATCAATCAATCTG 240  
 DB 304 ATTCTGACACACCCCGCTGCAATCTGTGTCCAGAGCGCAATATCACTGCTGTG 363  
 QY 241 ATCTCTGTAGCCCTTACCGCTGCAATCTGCTGCGCCGCAACCGCTCTCTCCG 300  
 DB 364 ACCCGAGTGAACCTTACAGTGGAGTCAAGTACGTGAGCAACCGCTTGAATACG 423  
 QY 301 ACCGACGTGATATGATGTGGGAGGCGCAACCTTATGCTCACTCTTATGAGAGAC 360  
 DB 424 AGTCATGTGACCTATTAAGTGGCGCGGCAATGCTGCTGCTTCACTGTGGTGAC 483  
 QY 361 CTGTGAGGCGCTATTTCTGTGTGGGAGGAGGTTCTCATGAGACATGCCCAATGG 420  
 DB 484 ATGTGTGGGGCTGTCTTCTGTGTGGGAGCAAGCTTCAAGTCAAGCTGTGCGCATCA 543  
 QY 421 ACTGTCCAGAGACTGCAACTGTT 443  
 DB 544 ACGGTCCAGACCTGTAACTGCTC 566

RESULT 13  
 ADP71119  
 ID ADP71119 standard; cDNA; 630 BP.  
 XX  
 AC ADP71119;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE HCV DNA encoding E1 protein HCC162.  
 XX  
 KW Hepatitis C virus; HCV; E1 glycoprotein; E2 glycoprotein; HCV infection;  
 KW liver disease; liver fibrosis; ss; serum alanine aminotransferase level;  
 KW steatosis; anti-E2 immunoreactivity; vaccine.  
 XX  
 OS Hepatitis C virus; type 3a.  
 XX  
 PN US2004126395-A1.  
 XX  
 PD 01-JUL-2004.  
 XX  
 PF 18-DEC-2002; 2002US-00321798.  
 XX  
 PR 18-DEC-2001; 2001US-0453708P.  
 XX  
 PR 16-OCT-2002; 2002US-0418358P.  
 XX  
 PA (MAER/) MAERTENS G.  
 XX  
 PA (DEPL/) DEPLA E.  
 XX  
 PA (BOSM/) BOSMAN F.  
 XX  
 PI Maertens G, Depla E, Bosman F;  
 XX  
 DR WPI; 2004-499089/47.  
 XX  
 DR P-PSDB; ADP71120.  
 XX  
 PT Use of hepatitis C virus (HCV) vaccine composition for reducing liver  
 XX disease, serum alanine aminotransferase levels, steatosis, or anti-E2  
 XX immunoreactivity in the liver of a chronic HCV-infected mammal.  
 XX  
 PS Example 2; SEQ ID NO 29; 176bp; English.  
 XX  
 CC The invention relates to the use of a hepatitis C virus (HCV) vaccine  
 CC composition for reducing liver disease (such as liver fibrosis or its  
 CC progression), serum alanine aminotransferase (ALT) levels, steatosis, or  
 CC anti-E2 immunoreactivity in the liver of a chronic HCV-infected mammal,  
 CC or for treating a chronic HCV-infected mammal. The liver disease is  
 CC reduced by at least 1-2 points according to the overall Ishak score in  
 CC the HCV-infected mammal. Also included are a method for predicting  
 CC changes in liver disease in a chronic HCV-infected mammal, a therapeutic  
 CC HCV vaccine composition (comprising at least one purified or a  
 CC combination of at least 2 HCV single or specific oligomeric recombinant  
 CC envelope protein selected from an E1 or E2 protein, a part of E1 and E2  
 CC proteins, an E1/E2 protein complex formed from purified HCV single or  
 CC specific oligomeric recombinant E1 or E2 proteins or its parts and  
 CC optionally a pharmaceutical adjuvant), a composition (comprising at least  
 CC one E1 or E2 peptide, and optionally, a pharmaceutical adjuvant), an  
 CC immunogenic HCV composition (or HCV vaccine composition) comprising a  
 CC recombinant virus allowing expression of at least one HCV recombinant  
 CC envelope protein (selected from an E1 protein and/or an E2 protein, and  
 CC their parts, and optionally, a pharmaceutical adjuvant) and an HCV  
 CC vaccine composition (comprising a recombinant virus allowing expression  
 CC of at least one HCV recombinant envelope protein chosen from an E1  
 CC protein and/or an E2 protein, and parts of the E1 and E2 proteins and,  
 CC optionally, a pharmaceutical adjuvant). The HCV vaccine composition is  
 CC useful for reducing liver disease (such as liver fibrosis or its  
 CC progression), serum ALT levels, steatosis, or anti-E2 immunoreactivity in  
 CC the liver in a chronic HCV-infected mammal, or for treating a chronic HCV  
 CC infected mammal, particularly human. The HCV E1 proteins are useful for  
 CC in vitro monitoring HCV disease or diagnosing the response to treatment  
 CC of patients suffering from HCV infection. The present sequence is an HCV  
 CC cDNA encoding an E1 protein (or fragment).  
 XX

Sequence 630 BP; 127 A; 175 C; 168 G; 160 T; 0 U; 0 Other;  
Query Match 52.1%; Score 233; DB 12; Length 630;  
Best Local Similarity 70.2%; Pred. No. 1,2e-62;  
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;  
QY 1 GACGGAATTAATTTGCAACAGGGAATTTACCTGTTGCTCTTCTATCTTCTCTG 60  
DB 124 GACGGGATTAATTTGCAACAGGGAATTTGCGGGTGTCTCTTCTATCTTCTCTG 183  
QY 61 GCTTTGTTCTATGCTTCTTACCCCAACAGCCGGGCTGAGTACCGTATGCTCCGA 120  
DB 184 GCTGTTCTCTTCTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 243  
QY 121 CTTCTAGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 180  
DB 244 CTTCTAGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 303  
QY 181 ATCTTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240  
DB 304 ATTTGTCACACACCGGCTGCAATTAATTAATTAATTAATTAATTAATTAATTAAT 363  
QY 241 ATCTTGTAGAGCCCTTACCGTCCGCTGAAAGTCCGCTGCGCCGACCGCTCTCCG 300  
DB 364 ACCCCAGTACACCTTACAGTGGCAGTCAAGTACGTCGAGCAACACCGCTTCAATAC 423  
QY 301 AGCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360  
DB 424 ATCTATGTGACCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 483  
QY 361 CTTTGTAGAGCCCTTATTTCTTGTGAGGAGGCTTCTCATGAGATGCGCAGATG 420  
DB 484 ATGTGTGGGGCTGTCTTCTCGTGGGACAAAGCTTCAAGCTTCAAGCTGTGTGCAATCA 543  
QY 421 ACTGTCCAGACTGCACTGTTTC 443  
DB 544 ACGTCCAGACCTGTAACTGCTC 566  
RESULT 14  
AAZ07658  
ID AAZ07658 standard; DNA; 1249 BP.  
XX  
AC AAZ07658;  
XX  
DT 20-MAR-2003 (revised)  
DT 08-NOV-1999 (first entry)  
DE HCV J1 NS domain consensus DNA sequence.  
XX  
KM Hepatitis C virus; HCV; J1; J7; HCV-1; non-A, non-B HCV; NANBH;  
KM HCV infection; vaccine; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN EP939128-A2.  
XX  
PD 01-SEP-1999.  
XX  
PF 17-SEP-1990; 99EP-00101746.  
XX  
PR 15-SEP-1989; 89US-00408045.  
PR 21-DEC-1989; 89US-00456142.  
PR 17-SEP-1990; 90EP-00310149.  
XX  
PA (OYAA/) OYA A.  
PA (CHIR ) CHIRON CORP.  
XX  
PI Miyamura T, Saito I, Houghton M, Weiner AJ, Han J, Kolberg JA;  
XX Cha T, Irvine BD;  
XX WPI; 1999-480843/41.  
XX

PT New Hepatitis C Virus isolates, useful for diagnosis of hepatitis  
PT infections and development of vaccines.  
XX  
PS Disclosure; Fig 14; 132pp; English.  
XX  
XX The invention provides two new isolates of hepatitis C virus (HCV), J1  
CC and J7. These two isolates comprise nucleotide and amino acid sequences  
CC that are distinct from the HCV isolate HCV-1. The nucleotide sequences  
CC may be used to detect non-A, non-B HCV (NANBH) polynucleotides by  
CC hybridization for diagnosis of NANBH infections. They may also be used to  
CC screen blood donors, donated blood and blood products for this infection.  
CC The isolates may also be used to isolate other naturally occurring  
CC variants of the virus. The polypeptides may be used as a vaccine for  
CC administration to patients to protect against infection with NANBH. The  
CC present sequence represents the NS1 domain consensus sequence of HCV  
CC isolates J1 and HCV-1. (Updated on 20-MAR-2003 to correct PR field.)  
CC (Updated on 20-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 1249 BP; 160 A; 282 C; 276 G; 206 T; 0 U; 325 Other;  
Query Match 49.5%; Score 221.4; DB 2; Length 1249;  
Best Local Similarity 54.6%; Pred. No. 7.2e-59;  
Matches 244; Conservative 83; Mismatches 120; Indels 0; Gaps 0;  
QY 1 GACGGAATTAATTTGCAACAGGGAATTTACCTGTTGCTCTTCTATCTTCTCTG 60  
DB 68 GACGGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 127  
QY 61 GCTTTGTTCTATGCTTCTTACCCCAACAGCCGGGCTGAGTACCGTATGCTCCGA 120  
DB 128 GCTTGTCTTCTTCTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 187  
QY 121 CTTCTAGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 180  
DB 188 MTWTAACAGTACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 247  
QY 181 ATCTTCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240  
DB 248 ATCTGTCACACCGGCTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 307  
QY 241 ATCTTGTAGAGCCCTTACCGTCCGCTGAAAGTCCGCTGCGCCGACCGCTCTCCG 300  
DB 308 GTAGCGMTSACCCCTTACAGTGGGAGGAGTGCAGTATGCTGCTGCTGCTGCTGCTGCT 367  
QY 301 AGCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360  
DB 368 CGTCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 427  
QY 361 CTTTGTAGAGCCCTTATTTCTTGTGAGGAGGCTTCTCATGAGATGCGCAGATG 420  
DB 428 CTTTGTAGAGCCCTTATTTCTTGTGAGGAGGCTTCTCATGAGATGCGCAGATG 487  
QY 421 ACTGTCCAGACTGCACTGTTTC 447  
DB 488 ACRRTYCARGRYTGAAYTGTCTWATC 514  
RESULT 15  
AAQ35072  
ID AAQ35072 standard; DNA; 565 BP.  
XX  
AC AAQ35072;  
XX  
DT 20-MAY-1993 (first entry)  
DE HCV envelope region nucleic acid.  
XX  
KM Envelope; region; type C; hepatitis; virus; HCV; vaccine; serum;  
KM non-A, non-B; amplify; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN JP04349885-A.  
XX







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OM nucleic - nucleic search, using BW model

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4236.302 Million cell updates/sec

Title: US-09-851-138c-51

Perfect score: 447  
Sequence: 1 gacgggaattcaatttcgcaac.....aggactcgaactgttcacac 447

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq: \*  
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4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/PCUS\_COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445.8	99.7	447	3	US-08-836-075A-51
2	236.2	52.8	541	4	US-09-878-281A-13
3	236.2	52.8	541	4	US-09-878-281A-17
4	234.6	52.5	541	4	US-09-878-281A-19
5	233	52.1	541	4	US-09-878-281A-15
6	233	52.1	541	4	US-09-878-281A-21
7	233	52.1	541	4	US-09-878-281A-25
8	233	52.1	541	4	US-09-878-281A-27
9	233	52.1	630	3	US-08-612-973-29
10	233	52.1	630	3	US-08-612-973-29
11	231.4	51.8	541	4	US-09-878-281A-23
12	217.4	48.6	579	4	US-09-878-281A-177
13	215.8	48.3	574	4	US-09-878-281A-120
14	215.8	48.3	579	4	US-09-878-281A-175
15	215.8	48.3	579	4	US-09-878-281A-181
16	209.8	46.9	447	3	US-08-836-075A-39
17	209	46.8	447	3	US-08-836-075A-31
18	208.6	46.7	447	3	US-08-836-075A-37
19	206.6	46.1	579	4	US-09-878-281A-173
20	206.2	46.2	579	4	US-09-878-281A-187
21	205	45.9	579	4	US-09-878-281A-171
22	204.6	45.8	574	4	US-09-878-281A-118
23	204.2	45.7	2116	3	US-08-191-160-21
24	203	45.4	579	4	US-09-878-281A-155
25	201.4	45.1	579	4	US-09-878-281A-155
26	201.4	45.1	579	4	US-09-878-281A-155
27	201	45.0	447	3	US-08-836-075A-29

28	199.4	44.6	742	1	US-08-081-072-18	Sequence 18, Appl
29	199.4	44.6	742	1	US-08-449-093A-18	Sequence 18, Appl
30	199.4	44.6	932	1	US-08-081-072-15	Sequence 15, Appl
31	199.4	44.6	932	1	US-08-449-093A-15	Sequence 15, Appl
32	198.2	44.3	447	3	US-08-836-075A-35	Sequence 35, Appl
33	197.8	44.3	447	3	US-08-836-075A-33	Sequence 33, Appl
34	196.2	43.9	501	2	US-08-483-695-30	Sequence 30, Appl
35	196.2	43.9	501	2	US-07-965-285-30	Sequence 30, Appl
36	196.2	43.9	501	2	US-08-487-231-30	Sequence 30, Appl
37	196.2	43.9	501	3	US-09-201-912-30	Sequence 30, Appl
38	196.2	43.9	633	3	US-08-612-973-7	Sequence 7, Appl1
39	196.2	43.9	633	3	US-08-927-597-7	Sequence 7, Appl1
40	196.2	43.9	795	3	US-08-612-973-5	Sequence 5, Appl1
41	196.2	43.9	795	3	US-08-927-597-5	Sequence 5, Appl1
42	196.2	43.9	2082	3	US-08-612-973-47	Sequence 47, Appl
43	196.2	43.9	2082	3	US-08-927-597-47	Sequence 47, Appl
44	196.2	43.9	2433	3	US-08-612-973-49	Sequence 49, Appl
45	196.2	43.9	2433	3	US-08-927-597-49	Sequence 49, Appl

#### ALIGNMENTS

RESULT 1  
US-08-836-075A-51

Sequence 51, Application US/08836075A

Patent No. 6180768

GENERAL INFORMATION:

APPLICANT: MAERTENS, GERT

APPLICANT: STUYVER, LIEVEN

TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES

TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC

NUMBER OF INVENTION: AGENTS

NUMBER OF SEQUENCES: 207

CORRESPONDENCE ADDRESSES:

ADDRESSEE: ARNOLD, WHITE & DURKEE

STREET: P.O. BOX 4433

CITY: HOUSTON

STATE: TEXAS

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word 6.0 / ASCII text output

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,075A

FILING DATE: 21 Apr 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/04155

FILING DATE: 23 Oct 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94870166.9

FILING DATE: 21 Oct 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95870076.7

FILING DATE: 28 Jun 1995

ATTORNEY/AGENT INFORMATION:

NAME: KAMMERER, PATRICIA A.

REGISTRATION NUMBER: 29,775

REFERENCE/DOCKET NUMBER: INNS:004

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 447 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-836-075A-51

Query Match 99.7%; Score 445.8; DB 3; Length 447;  
Best Local Similarity 100.0%; Pred. No. 1.7e-124;  
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTGCAACAGGGAATTTACCTGTTGCTCTTCTCTATCTTCTCTG 60  
DB 1 GACGGAATTAATTTGCAACAGGGAATTTACCTGTTGCTCTTCTCTATCTTCTCTG 60

QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCCGGCTGAGTACCGTAAATGCTCCGA 120  
DB 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCCGGCTGAGTACCGTAAATGCTCCGA 120

QY 121 CTCTACATGTAATCTACAGCTGCACTGAACGTAAGTATGATGAGCCGGGATATT 180  
DB 121 CTCTACATGTAATCTACAGCTGCACTGAACGTAAGTATGATGAGCCGGGATATT 180

QY 181 ATCTCTCACTTAACCTGCTGTGTCTCCCTGCGTAAGCTCTTGGAATATCAAGATGCTG 240  
DB 181 ATCTCTCACTTAACCTGCTGTGTCTCCCTGCGTAAGCTCTTGGAATATCAAGATGCTG 240

QY 241 ATCCCTGTAGCCCTTACCGCTCCGCTGGAAGTCCCTTGCGCCGACCGCTCTCCGC 300  
DB 241 ATCCCTGTAGCCCTTACCGCTCCGCTGGAAGTCCCTTGCGCCGACCGCTCTCCGC 300

QY 301 AGCAGCTGGAATATGATGTGGGCGGCAACCTATGCTCAAGCTCTACAGTGAAGAC 360  
DB 301 AGCAGCTGGAATATGATGTGGGCGGCAACCTATGCTCAAGCTCTACAGTGAAGAC 360

QY 361 CTTTGTGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATGAGACATGCGCAGATTG 420  
DB 361 CTTTGTGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATGAGACATGCGCAGATTG 420

QY 421 ACTGTCCAGACTGCAACTGTTCATC 447  
DB 421 ACTGTCCAGACTGCAACTGTTCATC 447

RESULT 2  
US-09-878-281A-13  
; Sequence 13, Application US/09878281A  
; Patent No. 6762024  
; GENERAL INFORMATION:  
; APPLICANT: Immunogenetics N.V.  
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph  
; FILE REFERENCE: 35  
; CURRENT APPLICATION NUMBER: US/09/878,281A  
; CURRENT FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 284  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 13  
; LENGTH: 541  
; TYPE: DNA  
; ORGANISM: hepatitis C virus  
US-09-878-281A-13

Query Match 52.8%; Score 236.2; DB 4; Length 541;  
Best Local Similarity 70.7%; Pred. No. 1.8e-61;  
Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTGCAACAGGGAATTTACCTGTTGCTCTTCTCTATCTTCTCTG 60  
DB 62 GACGGAATTAATTTGCAACAGGGAATTTGCTGCTCTTCTCTATCTTCTCTG 121

QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCCGGCTGAGTACCGTAAATGCTCCGA 120  
DB 122 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCTGAGTGGGGAACAGTCTGCG 181

QY 121 CTCTACATGTAATCTACAGCTGCACTGAACGTAAGTATGATGAGCCGGGATATT 180  
DB 122 CTCTACATGTAATCTACAGCTGCACTGAACGTAAGTATGATGAGCCGATGACGTT 241

QY 181 ATCTCTCACTTAACCTGCTGTGTCTCCCTGCGTAAGCTCTTGGAATATCAAGATGCTG 240

DB 242 ATTCTGCAACACCGGCTGTGTACTTGTGTTCAGAACGTAATATCTGCGTCTG 301

QY 241 ATCCCTGTAGCCCTTACCGCTCCGCTGGAAGTCCCTTGCGCCGACCGCTCTCTCCGC 300  
DB 302 ACCCGAGTACACCTTACAGTGGCACTGACGTACGTGAGGCAACACCGCTTCTGATCCG 361

QY 301 AGCAGCTGGAATATGATGTGGGCGGCAACCTATGCTCAAGCTCTACAGTGAAGAC 360  
DB 362 AGCAGCTGGAATATGATGTGGGCGGCAACGATGTCTGTCTCTTACAGTGGAT 421

QY 361 CTTTGTGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATGAGACATGCGCAGATTG 420  
DB 422 ATGTGTGGGCGCTTCTCTCTGTGGGCAAGCCTTCAAGTTCAGACCTGTGCGCATCA 481

QY 421 ACTGTCCAGACTGCAACTGTTC 443  
DB 482 ACTGTCCAGACTGCAACTGTTC 504

RESULT 3  
US-09-878-281A-17  
; Sequence 17, Application US/09878281A  
; Patent No. 6762024  
; GENERAL INFORMATION:  
; APPLICANT: Immunogenetics N.V.  
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph  
; FILE REFERENCE: 35  
; CURRENT APPLICATION NUMBER: US/09/878,281A  
; CURRENT FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 284  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 17  
; LENGTH: 541  
; TYPE: DNA  
; ORGANISM: hepatitis C virus  
US-09-878-281A-17

Query Match 52.8%; Score 236.2; DB 4; Length 541;  
Best Local Similarity 70.7%; Pred. No. 1.8e-61;  
Matches 313; Conservative 1; Mismatches 129; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTGCAACAGGGAATTTACCTGTTGCTCTTCTCTATCTTCTCTG 60  
DB 62 GACGGAATTAATTTGCAACAGGGAATTTGCTGCTCTTCTCTATCTTCTCTG 121

QY 61 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCCGGCTGAGTACCGTAAATGCTCCGA 120  
DB 122 GCTTTGTTCTCATGCTTGTCTTACACCCACAGCTGAGTGGGGAACAGTCTGCG 181

QY 121 CTCTACATGTAATCTACAGCTGCACTGAACGTAAGTATGATGAGCCGGGATATT 180  
DB 182 CTCTACATGTAATCTACAGCTGCACTGAACGTAAGTATGATGAGCCGATGACGTT 241

QY 181 ATCTCTCACTTAACCTGCTGTGTCTCCCTGCGTAAGCTCTTGGAATATCAAGATGCTG 240  
DB 242 ATCTCTCACTTAACCTGCTGTGTCTCCCTGCGTAAGCTCTTGGAATATCAAGATGCTG 301

QY 241 ATCCCTGTAGCCCTTACCGCTCCGCTGGAAGTCCCTTGCGCCGACCGCTCTCTCCGC 300  
DB 302 ACCCGAGTACACCTTACAGTGGCACTGACGTACGTGAGGCAACACCGCTTCTGATCCG 361

QY 301 AGCAGCTGGAATATGATGTGGGCGGCAACCTATGCTCAAGCTCTACAGTGAAGAC 360  
DB 362 AGCAGCTGGAATATGATGTGGGCGGCAACGATGTCTGTCTCTTACAGTGGAT 421

QY 361 CTTTGTGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATGAGACATGCGCAGATTG 420  
DB 422 ATGTGTGGGCGCTTCTCTCTGTGGGCAAGCCTTCAAGTTCAGACCTGTGCGCATCA 481

QY 421 ACTGTCCAGACTGCAACTGTTC 443

Db 482 ACGGTCCAGACCTGTAACTGCTC 504

## RESULT 4

US-09-878-281A-19  
; Sequence 19, Application US/09878281A  
; Patent No. 6762024  
; GENERAL INFORMATION:  
; APPLICANT: Immunogenetics N.V.  
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph  
; FILE REFERENCE: 35  
; CURRENT APPLICATION NUMBER: US/09/878,281A  
; NUMBER OF SEQ ID NOS: 284  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 541  
; TYPE: DNA  
; ORGANISM: hepatitis C virus  
US-09-878-281A-19

Query Match 52.5%; Score 234.6; DB 4; Length 541;  
Best Local Similarity 70.4%; Pred. No. 5,5e-61;  
Matches 312; Conservative 1; Mismatches 130; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTGCGCAACAGGAAATTTAACTGTTGCTCTTTCCTATCTTCTCTG 60  
DB 62 GACGGGATTAATTGCGCAACAGGAAATTTGCGGTTGCTCTTTCCTATCTTCTCTG 121  
QY 61 GCTTTGTTCTCATGCTGCTTACCAACGCGGGCTGAGAACCGTAATGCTCCGGA 120  
DB 122 GCTGTGTTCTCTTCTTAATTCATCCAGACGTAAGTGGGGAATACGTTGCG 181  
QY 121 CTCTACATGTAATTAACGACGCTGAGTAAGTAGTATGAGGCGGGAATATT 180  
DB 182 CTCTATGCTCTTACCAACGACGCTTCCATAGACAGTATGTGACAGGCCATGACGT 241  
QY 181 ATCTTCACCTTACCTGCTGCTGTGCTCCCTGCGTAACGCTTGGCAATACATCAAGACTGG 240  
DB 242 ATTCTGCACACACCGGCTGACATACCTTGTGTCAGAGACGGAATACATCAGTCTGG 301  
QY 241 ATCCCTGTAGACCCCTAACCGTCCGCTGGAAGTCCGCTGCGCCGACCGCTCTCCCG 300  
DB 302 ACCCGCATGACACCTTACAGTGGAGTCAAGTACGTGGAGCAACCGCTTGATACGC 361  
QY 301 ACGCAGTGGATATGATGAGTGGGCGGCGCACCTATGCTCAGCTCTCTACGTAGAGAC 360  
DB 362 AGTCAATGTGACCTATTAAGTGGCGCGGCCACATGTCTCAGCGCTCTACGTGGTGA 421  
QY 361 CTTTGTGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATGAGACATGCGCAGATTGG 420  
DB 422 ATGTGAGGGGCGCTCTTCTTGTGGGCAAGCCTTCACGTTCAAGCTGTGCCATCA 481  
QY 421 ACTGTCCAGACGTGCAACTGTTTC 443  
DB 482 ACGGTCCAGACCTGTAACTGCTC 504

## RESULT 5

US-09-878-281A-15  
; Sequence 15, Application US/09878281A  
; Patent No. 6762024  
; GENERAL INFORMATION:  
; APPLICANT: Immunogenetics N.V.  
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph  
; FILE REFERENCE: 35  
; CURRENT APPLICATION NUMBER: US/09/878,281A  
; NUMBER OF SEQ ID NOS: 284  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15

; LENGTH: 541  
; TYPE: DNA  
; ORGANISM: hepatitis C virus  
US-09-878-281A-15

Query Match 52.1%; Score 233; DB 4; Length 541;  
Best Local Similarity 70.2%; Pred. No. 1.7e-60;  
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTGCGCAACAGGAAATTTAACTGTTGCTCTTTCCTATCTTCTCTG 60  
DB 62 GACGGGATTAATTGCGCAACAGGAAATTTGCGGTTGCTCTTTCCTATCTTCTCTG 121  
QY 61 GCTTTGTTCTCATGCTGCTTACCAACGCGGGCTGAGAACCGTAATGCTCCGGA 120  
DB 122 GCTGTGTTCTCTTCTTAATTCATCCAGACGTAAGTGGGGAATACGTTGCG 181  
QY 121 CTCTACATGTAATTAACGACGCTGAGTAAGTAGTATGAGGCGGGAATATT 180  
DB 182 CTCTATGCTCTTACCAACGACGCTTCCATAGACAGTATGTGACAGGCCATGACGT 241  
QY 181 ATCTTCACCTTACCTGCTGTGCTCCCTGCGTAACGCTTGGCAATACATCAAGACTGG 240  
DB 242 ATTCTGCACACACCGGCTGACATCTGTGTTACAGACGTAATACATCTGCTGG 301  
QY 241 ATCCCTGTAGACCCCTAACCGTCCGCTGGAAGTCCGCTGCGCCGACCGCTCTCCCG 300  
DB 302 ACCCGCATGACACCTTACAGTGGAGTCAAGTACGTGGAGCAACCGCTTGATACGC 361  
QY 301 ACGCAGTGGATATGATGAGTGGGCGGCGCACCTATGCTCAGCTCTCTACGTAGAGAC 360  
DB 362 AGTCAATGTGACCTATTAAGTGGCGCGGCCACATATGTCTCTCTCTACGTGGTGA 421  
QY 361 CTTTGTGAGCGCTATTTCTTGTGGGCAAGGGTTCTCATGAGACATGCGCAGATTGG 420  
DB 422 ATGTGAGGGGCGCTCTTCTTGTGGGCAAGCCTTCACGTTCAAGCTGTGCCATCA 481  
QY 421 ACTGTCCAGACGTGCAACTGTTTC 443  
DB 482 ACGGTCCAGACCTGTAACTGCTC 504

## RESULT 6

US-09-878-281A-21  
; Sequence 21, Application US/09878281A  
; Patent No. 6762024  
; GENERAL INFORMATION:  
; APPLICANT: Immunogenetics N.V.  
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph  
; FILE REFERENCE: 35  
; CURRENT APPLICATION NUMBER: US/09/878,281A  
; NUMBER OF SEQ ID NOS: 284  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 541  
; TYPE: DNA  
; ORGANISM: hepatitis C virus  
US-09-878-281A-21

Query Match 52.1%; Score 233; DB 4; Length 541;  
Best Local Similarity 70.2%; Pred. No. 1.7e-60;  
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTGCGCAACAGGAAATTTAACTGTTGCTCTTTCCTATCTTCTCTG 60  
DB 62 GACGGGATTAATTGCGCAACAGGAAATTTGCGGTTGCTCTTTCCTATCTTCTCTG 121  
QY 61 GCTTTGTTCTCATGCTGCTTACCAACGCGGGCTGAGTAAGTATGCTCCGGA 120  
DB 122 GCTGTGTTCTCTTCTTAATTCATCCAGACGTAAGTGGGGAATACGTTGCG 181

121 CTCATCATGTAATTAACAGTACAGTACAGTAAGTATGATGAGCCGGGATATT 180  
182 CTCATGCTCTTAACCAACAGTCTTCCAAATAGAGATTTGTACAGAGCCGATGACGTT 241  
181 ATCTCCACTTAACCTGCTGTGTGCTCCCTGCGTAAGCTCTGCGCAATACATCAAGATCTGG 240  
242 ATTCTGACACACCCGGCTGCAATACCTTGTGTGTCAGAGACGGCAATACATCAGTCTGG 301  
241 ATCCCTGTAGCCGTAACGCTGCGGTGAAGTGCCTGTGCGCGCCGACCGCTCTCCGC 300  
302 ACCCGAGTAACCTTAACAGTGGAGTCAAGTACGTGGAGCAACACCGCTTCGATACGC 361  
301 ACCGACGTGATATGATGTGGGAGCGGACCCCTAATGCTCTCACTTACAGTACAGAC 360  
362 AGTCATGTGACCTTATTAATGAGCGGCGGCAAGATGTGCTCTGCTTACAGTGGTAC 421  
361 CTTTGTGAGCGGCTATTCTTGTGGGCAAGGGTCTCATGAGACATGCGCAGCATGG 420  
422 ATGTGTGGGGCTGTCTCTCCGTGGGCAAGCCTTACGTTCAAGCCTGCTGCGCATCAA 481  
421 ACTGTCCAGACCTGCAACTGTTTC 443  
482 ACGGTCCAGACCTGTAACTGCTC 504

## RESULT 7

US-09-878-281A-25  
; Sequence 25, Application US/09878281A  
; Patent No. 6762024  
; GENERAL INFORMATION:  
; APPLICANT: Immunogenetics N.V.  
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph  
; TITLE OF INVENTION: and therapy  
; FILE REFERENCE: 35  
; CURRENT APPLICATION NUMBER: US/09/878,281A  
; CURRENT FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 284  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 541  
; TYPE: DNA  
; ORGANISM: hepatitis C virus  
US-09-878-281A-25

Query Match 52.1%; Score 233; DB 4; Length 541;

Best Local Similarity 70.2%; Pred. No. 1.7e-60;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

1 GACGGAATTAATTTGCAACAGGGAATTTACCTGCTGCTTTCTATCTTCTCTG 60  
62 GACGGGATTAACCTTGCAACAGGGAATTTGCCGGTGTGCTTTTCTATCTTCTCTT 121  
61 GCTTGTCTCATGCTTGTCTTACACCAAGCGGCTGAGTACCTGATGCTCCGGA 120  
122 GCTGTGTTCTCTGCTTAATTCATCCAGAGCTGTGCTAGAGTGGCGGAATGCTGAC 181  
121 CTCATCATGTAATTAACAGTACAGTACAGTAAGTATGATGAGCCGGGATATT 180  
182 CTCATGCTCTTAACCAACAGTCTTCCAAATAGTATGTATGAGGCCGATGACGTT 241  
181 ATCTCCACTTAACCTGCTGTGTGCTCCCTGCGTAAGCTCTGCGCAATACATCAAGATCTGG 240  
242 ATTCTGACACCGCGGCTGTGTAACCTTGTGTGTCAGAGACGGCAATACGTTACATGCTGG 301  
241 ATCCCTGTAGCCGTAACGCTGCGGTGAAGTGCCTGTGCGCGCCACCGCTCTCTCCGC 300  
302 ACCCGAGTAACCTTAACAGTGGAGTCAAGTACGTGGAGCAACACCGCTTCGATACGC 361  
301 ACCGACGTGATATGATGTGGGAGCGGACCCCTAATGCTCTCACTTACAGTACAGAC 360  
362 AGTCATGTGACCTTATTAATGAGCGGCGGCAAGATGTGCTCTGCTTACAGTGGTAC 421  
361 CTTTGTGAGCGGCTATTCTTGTGGGCAAGGGTCTCATGAGACATGCGCAGCATGG 420

422 ATGTGTGGGGCCGCTTCTCTGTTGGACAGAGCTTCAAGTTACAGACCCGCGCATCAA 481  
421 ACTGTCCAGACCTGCAACTGTTTC 443  
482 ACGGTCCAGACCTGTAACTGCTC 504

## RESULT 8

US-09-878-281A-27  
; Sequence 27, Application US/09878281A  
; Patent No. 6762024  
; GENERAL INFORMATION:  
; APPLICANT: Immunogenetics N.V.  
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph  
; TITLE OF INVENTION: and therapy  
; FILE REFERENCE: 35  
; CURRENT APPLICATION NUMBER: US/09/878,281A  
; CURRENT FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 284  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 541  
; TYPE: DNA  
; ORGANISM: hepatitis C virus  
US-09-878-281A-27

Query Match 52.1%; Score 233; DB 4; Length 541;

Best Local Similarity 70.2%; Pred. No. 1.7e-60;

Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;

1 GACGGAATTAATTTGCAACAGGGAATTTACCTGCTGCTTTCTATCTTCTCTG 60  
62 GACGGGATTAACCTTGCAACAGGGAATTTGCCGGTGTGCTTTTCTATCTTCTCTT 121  
61 GCTTGTCTCATGCTTGTCTTACACCAAGCGGCTGAGTACCTGATGCTCCGGA 120  
122 GCTGTGTTCTCTGCTTAATTCATCCAGAGCTGTGCTAGAGTGGCGGAATGCTGAC 181  
121 CTCATCATGTAATTAACAGTACAGTACAGTAAGTATGATGAGCCGGGATATT 180  
182 CTCATGCTCTTAACCAACAGTCTTCCAAATAGTATGTATGAGGCCGATGACGTT 241  
181 ATCTCCACTTAACCTGCTGTGTGCTCCCTGCGTAAGCTCTGCGCAATACATCAAGATCTGG 240  
242 ATTCTGACACCGCGGCTGTGTAACCTTGTGTGTCAGAGACGGCAATACGTTACATGCTGG 301  
241 ATCCCTGTAGCCGTAACGCTGCGGTGAAGTGCCTGTGCGCGCCACCGCTCTCTCCGC 300  
302 ACCCGAGTAACCTTAACAGTGGAGTCAAGTACGTGGAGCAACACCGCTTCGATACGC 361  
301 ACCGACGTGATATGATGTGGGAGCGGACCCCTAATGCTCTCACTTACAGTACAGAC 360  
362 AGTCATGTGACCTTATTAATGAGCGGCGGCAAGATGTGCTCTGCTTACAGTGGTAC 421  
361 CTTTGTGAGCGGCTATTCTTGTGGGCAAGGGTCTCATGAGACATGCGCAGCATGG 420  
422 ATGTGTGGGGCCGCTTCTCTGTTGGACAGAGCTTCAAGCTTCAAGACCCGCGCATCAA 481  
421 ACTGTCCAGACCTGCAACTGTTTC 443  
482 ACGGTCCAGACCTGTAACTGCTC 504

## RESULT 9

US-08-612-973-29  
; Sequence 29, Application US/08612973  
; Patent No. 6150134  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GERT  
; APPLICANT: BOSMAN, FONS  
; APPLICANT: DE MARTINOPE, GUY  
; APPLICANT: BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE  
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,973  
FILING DATE: 11-MAR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 630 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..624  
NAME/KEY: mat peptide  
LOCATION: 1..624  
US-08-612-973-29

Query Match 52.1%; Score 233; DB 3; Length 630;  
Best Local Similarity 70.2%; Pred. No. 1.8e-60;  
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;  
QY 1 GAGGAAATTAATTTGCAACAGGAAATTTACCTGCTTCTCTATCTCTCTG 60  
DB 124 GAGGGATAAATTTGCAACAGGAAATTTGCGGTTGCTCTTCTATTTCTCTTC 183  
QY 61 GCTTTGTTCTCATGCTTGTCTTACCAACCAAGCGGCTGAGTACGTAATGCTCCGA 120  
DB 184 GCTCTGTTCTCTGCTTAATTTATTCAGAGCTAGTCTAAGTGGCGAATAGTCTGGC 243  
QY 121 CTCTACATGTAATTAACGAGCTCAAGTACGTAATGTAATGAGCGGAGATATT 180  
DB 244 CTCTAGTCTCTTACCAACGAGCTGTTCCATAGCAATGTAATGTAACGAGCGGATG 303  
QY 181 ATCTGCACTTACCTGCTGTGTCCCTGAGTACGCTCTGCAATCATCAAGATGCTG 240  
DB 304 ATTCTGACACACCGGCTGCATACCTTGTGTCAGAGCGCAATATCATCATGCTGG 363  
QY 241 ATCTGAGACCCYACCGTGCCTGTAAGTGCCTGCGCGCAACGCTCTCTCTCGC 300  
DB 364 ACCCAAGTACACCTACAGTGGCAGTCAATAGTGGAGCAACCGCTTGATACGC 423  
QY 301 ACCGAGTGAATGATGTTGGGCGGCGCAACCTATGCTCAGTCTCTACGTAAGAGAC 360  
DB 424 AGTCAATGAGACCTAATGAGGCGCGCGCAACATGCTCTGCGCTCTACGTTGGTGAC 483  
QY 361 CTGTGAGAGCGGATTTCTGTGTGGGAGGAGGTTCTCATGAGACATGCGACATGG 420

DB 484 ATGTGAGGCGCTGTCTTCTGTTGGAGACAGCTTACGTTACAGCTGTGCGCATCA 543  
QY 421 ACTGTCAGAGCTGCACTGTTTC 443  
DB 544 ACGGTCAGACCTGTAATGCTTC 566  
RESULT 10  
US-08-927-597-29  
Sequence 29, Application US/08927597  
Patent No. 624503  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT  
APPLICANT: BOSMAN, FONS  
APPLICANT: DE MARTINOFF, GUY  
APPLICANT: BUYS, MARIE-ANGE  
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/612,973  
FILING DATE: 11-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 630 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..624  
NAME/KEY: mat peptide  
LOCATION: 1..624  
US-08-927-597-29  
Query Match 52.1%; Score 233; DB 3; Length 630;  
Best Local Similarity 70.2%; Pred. No. 1.8e-60;  
Matches 311; Conservative 1; Mismatches 131; Indels 0; Gaps 0;  
QY 1 GAGGAAATTAATTTGCAACAGGAAATTTACCTGCTTCTCTATCTCTCTG 60  
DB 124 GAGGGATAAATTTGCAACAGGAAATTTGCGGTTGCTCTTCTATTTCTCTTC 183  
QY 61 GCTTTGTTCTCATGCTTGTCTTACCAACCAAGCGGCTGAGTACGTAATGCTCCGA 120  
DB 184 GCTCTGTTCTCTGCTTAATTTATTCAGAGCTAGTCTAAGTGGCGAATAGTCTGGC 243



Oy	121	CTCTACATGGTAACTGACACGACTGACAGTAAACGGTAGTATGCTGTATATGAGCCGGGGATATT	180
Db	244	CTCTATATGCTCTTACCAACGACCTGTTCCAAATAGCAGTATTTGTATCAAGGCCATGACGTT	303
Oy	181	ATCTCTCACTTAACCTGGCTGTGTCTCCCTTCGTAACGCTCTGGCAATACATCAAGATCCTGG	240
Db	304	ATTCTGCACACACCCGGCTGCATACCTTGTGTGCAGAGACGGCAATATCATCAAGTCTGG	363
Oy	241	ATCCCTGTAGAGCCCAACGCTGCACCGTAGAGTGCCCTGGACGCCCAACCGCCTCTCTCCGC	300
Db	364	AACCCAGTGAACACTTACAGATGGGCAATGACAGTAAAGTACGAGCAACCAACCGTTTGATACGC	423
Oy	301	ACGCACCTGGAGATATGATGTGGGAGCGGCGCAACCTATGCTCAGCTCTTACAGTAGAGAC	360
Db	424	AGTACATGTGAGACCTTATGATGTGGACCGGGCACAGATGTGCTTCGGCGCTTACAGGGGTGAC	483
Oy	361	CTTGTGTGAGCGCCTATTTCTTGTGGGCGAGGGGTTCTCATGAGACATGCGCCACATTTGG	420
Db	484	ATGTGTGGGGGCTGTCTCTCGTGGGACAAAGCCTTACGTTTACAGACTGTGGCCATCAA	543
Oy	421	ACTGTCCAGACTGCACATGTTCT	443
Db	544	AAGGTCCAGACTGTAACTGCTC	566

```

RESULT 11
US-09-878-281A-23
; Sequence 23, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy
; TITLE OF INVENTION: and therapy
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878,281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 541
; TYPE: DNA
; ORGANISM: hepatitis C virus
; US-09-878-281A-23

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	Query Match	Similarity	51.8%	Score 231.4	DB 4	Length 541
	Best Local	Similarity 70.0%	Pred. No. 5.1e-60			
	Matches 310	Conservative 1	Mismatches 132	Indels 0	Gaps 0	
QY	1	GACGGAAATTAATTTGGCAACAGAGGAATTAACCTGGTGTCTCTTCTTCTATCTCTCTTCG	60			
Db	62	GACGGGAATAAAGCTTGGCAACAGGAATTTGCCGGGTGCTCTTTCTATCTCTCTCTT	121			
QY	61	GCTTGTGTCTCATGCTTGCTTAACCCACAGCCGGGCTGGAGTACCGTATATGCTTCGGA	120			
Db	122	GCTCTGTTCTCTTGGCTTAATCATCATCAGACGCTGGCTTAAGATGGGGAAATACGTCTGAC	181			
QY	121	CTTACATAGTAACTACAGACCTGCAGATAACGGTAGATGTGTATATAGGACCGGGATATT	180			
Db	182	CTTAATGTCTTACCAAGACCTGTTCCAAATAGATATGTATATAGGACCAATGACGTT	241			
QY	181	ATCTCCACTTAACCTGGCTGTGTCCCTGCAGTACGCTTCGGAAATCATCAAGATCTGG	240			
Db	242	ATTCTGCACGGGCCGGCTGTGTACTTGTGTCTCAAGAACGGCAATACGTCTACATCTGG	301			
QY	241	ATCCTGTGAGCCYTAACCGTCGCCGTGAAGTGCCTCGCGCCACACGGCTCTCTCCGC	300			
Db	302	ACCCCAAGTAACCTTAACAGTGCACATCAGGTACGTCTGGGGCAACACCGCTTCGATAACGC	361			
QY	301	ACGCACGGGAATATATGTGTGGGAGCGGCACACCTATGCTCAGCTCTCAACGATAGAAC	360			
Db	362	AGTATATGGAACTCTGTATGTAGAGCGCGGCACGAATGTGCTTCGGCTTTACGTGGGTAT	421			

Oy 361 CTTGTGGAGGGCATTTCTTGTVGGGAGGGGTTCTCATGGAGCATGCGCAGCATTGG 420  
 Db 422 ATGTGTGGGGCGCTTCTCTCGTGGGACAAAGCTTCAAGTTCAAGACCCCGCCGCTCAA 481  
 Oy 421 ACTGTCCAGACTGCACACTTTC 443  
 Db 482 ACGGTCCAGACCTGTAACTGCTC 504

```

RESULT 12
US-09-878-281A-177
: Sequence 177, Application US/09878281A
: Patent No. 6762024
: GENERAL INFORMATION:
: APPLICANT: Immunogenetics N.V.
: TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy
: TITLE OF INVENTION: and therapy
: FILE REFERENCE: 35
: CURRENT APPLICATION NUMBER: US/09/878,281A
: CURRENT FILING DATE: 2001-06-12
: NUMBER OF SEQ ID NOS: 284
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 177
: LENGTH: 579
: TYPE: DNA
: ORGANISM: hepatitis C virus
US-09-878-281A-177

```

Query Match	48.6%	Score 217.4;	DB 4;	Length 579;
Best Local Similarity	67.6%	Pred. No. 8.4e-56;		
Matches 302; Conservative	2;	Mismatches 143;	Indels 0;	Gaps 0

Qy	1	GAGGGAATTAATTGGCAACAGGGGAATTAACGTGGTGTGCTTTGTCTATCTTCCGTCG	60
Dp	100	GAGGGGATCAATTAGCAGACAGGGAACTTCCGGCTGTCTTTTCTATCTTCCCTTGG	159
Qy	61	GCTTGTGTTCTCATGCTTGCTTACCCACAGCCGGGCTGAGTACCGTAATGCTCCGGA	120
Dp	160	GTACTTCTCTGCGCGCTAACTGTCCAGACGTCGTCTCAGCACTACCGGAATGCATGGGGC	219
Qy	121	CTTACATGTGTAACTTAAGACTGCAGTAAAGGTATATCTGTATAGAAGCCGGGATATT	180
Dp	220	ATCTAACCATGTGCACCMAGACTGCCCGAATCTCCAAATTGTGTATGAAGCCCAACCATCAC	279
Qy	181	ATCTCCCACTTAACGTGCTGTGTCCCTGCGCTAACGCTTGCAATACATCAAGATGCTGG	240
Dp	280	ATCATGACCTTACCCGGGTGTGTGTGCTCTGTGTAAATGTAAGAAATGTCTCGGGTTGCTGG	339
Qy	241	ATCCCTGTGAGCCCTAACCGTGTGCGCGGTGAATGTGCGCTTCGCGCCACCGCTCTCTCGGC	300
Dp	340	ATTTCTTTTAAACCCCACTGTAGCGGTGCCCTTACCTTCGGGGGCTCCACTTAACGTCTGTACCG	399
Qy	301	ACGCACGTGATATGATGTGTGGGAGCGGCGCACCCGTAATCTCTACGCTCTACGTAGAGAC	360
Dp	400	CAGCATGTGGACCTGATGTGTGGGGCGGCGCACTTATGTCTTCCCTTACATCGAGAGC	459
Qy	361	CTTTGTGAGAGCGCTAATTTCTGTGTGGGCAAGGGGTTCTCATGAGACATTCGCGCAGATTGG	420
Dp	460	CATTGCGGAGGTGTCTTCTTGGCAGGGGCAATGTGTCAATTCGTAACCCCGGCGTCAATTGG	519
Qy	421	ACTGTCCAGACCTGCACACTGTTCATC	447
Dp	520	ACTTACCCAGATGTCAACTGTGTTCATC	546

```

RESULT 13
US-09-878-281A-120
; Sequence 120, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy
; TITLE OF INVENTION: and therapy

```

FILE REFERENCE: 35  
CURRENT APPLICATION NUMBER: US/09/878,281A  
CURRENT FILING DATE: 2001-06-12  
NUMBER OF SEQ ID NOS: 284  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 120  
LENGTH: 574  
TYPE: DNA  
ORGANISM: hepatitis C virus  
US-09-878-281A-120

Query Match 48.3%; Score 215.8; DB 4; Length 574;  
Best Local Similarity 67.3%; Pred. No. 2.5e-55;  
Matches 301; Conservative 2; Mismatches 144; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGACAGGGAATTACCTGTTGCTCTTCTATCTTCTCTG 60  
DB 100 GACGGAATTAATTTCGACAGGGAATTTCCTCGGTGCTCTTCTATCTTCTCTA 159  
QY 61 GCTTTGTTCTATGCTTGTCTTACACCCAGCCGGCTGAGTACCTGTAATGCTCCGA 120  
DB 160 GCACTTCTCTCGTGTGCTTGAAGTCCGGCTCGGCGAGACATACCGAATCTCGGC 219  
QY 121 CTCTACATGTAATTAACAGACTGAGTACGTAATGTAATGTAATGAGCCGGGATATT 180  
DB 220 ATTATACAGTACCAATGATGCTCCGAACTCTAGTATGATGATGAGCTGACATCAT 279  
QY 181 ATCTCCACTTACCTGAGCTGTGTCCTGCTGTAAGCTCTGGAATACATGATGCTGG 240  
DB 280 ATCATGATCTACAGGAGTGTGCTTGTGCTGAGAAACCGGAACACCTGCGCTGCG 339  
QY 241 ATCCCTGTAGCCCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
DB 340 GTTCTCTTAAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 399  
QY 301 ACAGAGTGAATTAATGATGAGGAGGAGCCACTTATGCTGCTGCTGCTGCTGCTG 360  
DB 400 CGGACGTGATTAATGATGAGGAGGAGCCACTTATGCTGCTGCTGCTGCTGCTG 459  
QY 361 CTTTGTGAGCGCTATTTCTTGTGAGGAGGAGGTTCTCATGAGATGCGGCAATTGG 420  
DB 460 CTTTGTGAGGAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519  
QY 421 ACTGTCCAGAGCTGCACTGCTTCATC 447  
DB 520 ACTACCCAGAGCTGCACTGCTTCATC 546

## RESULT 14

US-09-878-281A-175  
Sequence 175, Application US/09878281A  
Patent No. 6762024  
GENERAL INFORMATION:  
APPLICANT: Innogenetics N.V.  
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy  
FILE REFERENCE: 35  
CURRENT APPLICATION NUMBER: US/09/878,281A  
CURRENT FILING DATE: 2001-06-12  
NUMBER OF SEQ ID NOS: 284  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 175  
LENGTH: 579  
TYPE: DNA  
ORGANISM: hepatitis C virus  
US-09-878-281A-175

Query Match 48.3%; Score 215.8; DB 4; Length 579;  
Best Local Similarity 67.3%; Pred. No. 2.5e-55;  
Matches 301; Conservative 2; Mismatches 144; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGACAGGGAATTACCTGTTGCTCTTCTATCTTCTCTG 60  
DB 100 GACGGAATTAATTTCGACAGGGAATTTCCTCGGTGCTCTTCTATCTTCTCTA 159  
QY 61 GCTTTGTTCTATGCTTGTCTTACACCCAGCCGGCTGAGTACCTGTAATGCTCCGA 120  
DB 160 GCACTTCTCTCGTGTGCTTGAAGTCCGGCTCGGCGAGACATACCGAATCTCGGC 219  
QY 121 CTCTACATGTAATTAACAGACTGAGTACGTAATGTAATGTAATGAGCCGGGATATT 180  
DB 220 ATTATACAGTACCAATGATGCTCCGAACTCTAGTATGATGATGAGCTGACATCAT 279  
QY 181 ATCTCCACTTACCTGAGCTGTGTCCTGCTGTAAGCTCTGGAATACATGATGCTGG 240  
DB 280 ATCATGATCTACAGGAGTGTGCTTGTGCTGAGAAACCGGAACACCTGCGCTGCG 339

DB 100 GACGGAATTAATGATGAGGGAATTTCCTCGGTGCTCTTCTATCTTCTCTA 159  
QY 61 GCTTTGTTCTATGCTTGTCTTACACCCAGCCGGCTGAGTACCTGTAATGCTCCGA 120  
DB 160 GCACTTCTCTCGTGTGCTTGAAGTCCGGCTCGGCGAGACATACCGAATCTCGGC 219  
QY 121 CTCTACATGTAATTAACAGACTGAGTACGTAATGTAATGTAATGAGCCGGGATATT 180  
DB 220 ATTATACAGTACCAATGATGCTCCGAACTCTAGTATGATGATGAGCTGACATCAT 279  
QY 181 ATCTCCACTTACCTGAGCTGTGTCCTGCTGTAAGCTCTGGAATACATGATGCTGG 240  
DB 280 ATCATGATCTACAGGAGTGTGCTTGTGCTGAGAAACCGGAACACCTGCGCTGCG 339  
QY 241 ATCCCTGTAGCCCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
DB 340 GTTCTCTTAAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 399  
QY 301 ACAGAGTGAATTAATGATGAGGAGGAGCCACTTATGCTGCTGCTGCTGCTGCTG 360  
DB 400 CGGACGTGATTAATGATGAGGAGGAGCCACTTATGCTGCTGCTGCTGCTGCTG 459  
QY 361 CTTTGTGAGCGCTATTTCTTGTGAGGAGGAGGTTCTCATGAGATGCGGCAATTGG 420  
DB 460 CTTTGTGAGGAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519  
QY 421 ACTGTCCAGAGCTGCACTGCTTCATC 447  
DB 520 ACTACCCAGAGCTGCACTGCTTCATC 546

## RESULT 15

US-09-878-281A-181  
Sequence 181, Application US/09878281A  
Patent No. 6762024  
GENERAL INFORMATION:  
APPLICANT: Innogenetics N.V.  
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy  
FILE REFERENCE: 35  
CURRENT APPLICATION NUMBER: US/09/878,281A  
CURRENT FILING DATE: 2001-06-12  
NUMBER OF SEQ ID NOS: 284  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 181  
LENGTH: 579  
TYPE: DNA  
ORGANISM: hepatitis C virus  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (152)..(152)  
OTHER INFORMATION: "n" is any nucleotide  
US-09-878-281A-181

Query Match 48.3%; Score 215.8; DB 4; Length 579;  
Best Local Similarity 67.5%; Pred. No. 2.5e-55;  
Matches 301; Conservative 1; Mismatches 144; Indels 0; Gaps 0;

QY 1 GACGGAATTAATTTCGACAGGGAATTACCTGTTGCTCTTCTATCTTCTCTG 60  
DB 100 GACGGAATTAATTTCGACAGGGAATTTCCTCGGTGCTCTTCTATCTTCTCTA 159  
QY 61 GCTTTGTTCTATGCTTGTCTTACACCCAGCCGGCTGAGTACCTGTAATGCTCCGA 120  
DB 160 GCACTTCTCTCGTGTGCTTGAAGTCCGGCTCGGCGAGACATACCGAATGCTCGGC 219  
QY 121 CTCTACATGTAATTAACAGACTGAGTACGTAATGTAATGTAATGAGCCGGGATATT 180  
DB 220 ATTATACAGTACCAATGATGCTCCGAACTCTAGTATGATGATGAGCTGACATCAT 279  
QY 181 ATCTCCACTTACCTGAGCTGTGTCCTGCTGTAAGCTCTGGAATACATGATGCTGG 240  
DB 280 ATCATGATCTACAGGAGTGTGCTTGTGCTGAGAAACCGGAACAGTTTCGCGCTGCG 339

```

Qy      241 ATCCCTGTGAGCCCTYACCGTGCCTGGAATGCGCCCTGCGCCGCCACCGCCTCTCTCCGC 300
Db      340 GTATCTCTGACACCTTACTGTGCTGCTCCCTACTGTGGGGCTCCGCTTACGTGCTACGG 399
Qy      301 ACGCACGTGGATATGATGATGGGAGCGGCGCACCTATGCTCAGCTCTCTACGTAGGAGAC 360
Db      400 CGGCAATGTGATTTGATGATGGGTGACGACACCTTGTCTGTGCCCTTACGTGGAGAC 459
Qy      361 CTTTGTGAGCGCCTATTTCTTGTGTGGGCGAGGGTTCTCATGAGACATGCCAGCATTTGG 420
Db      460 CTCTGTGGAGGTGTCTTCTTAGTGGGACAGATGTTCACTTCAGCGCGCGCCACTGG 519
Qy      421 ACTGTCAGGACTGCAACTGTTCCAT 446
Db      520 ACCACTCAGGACTGCNACTGCTCCAT 545

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Search completed: December 29, 2004, 16:01:13  
 Job time : 82 secs